

Fig. 1.0

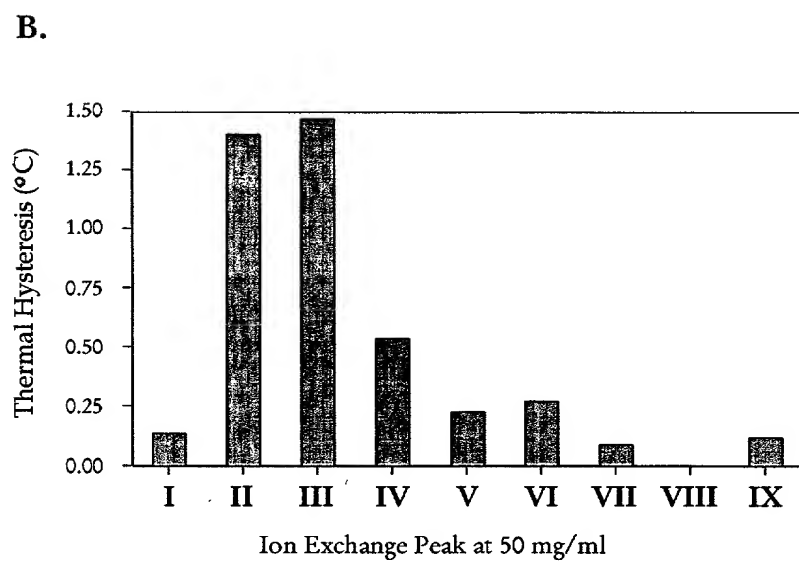
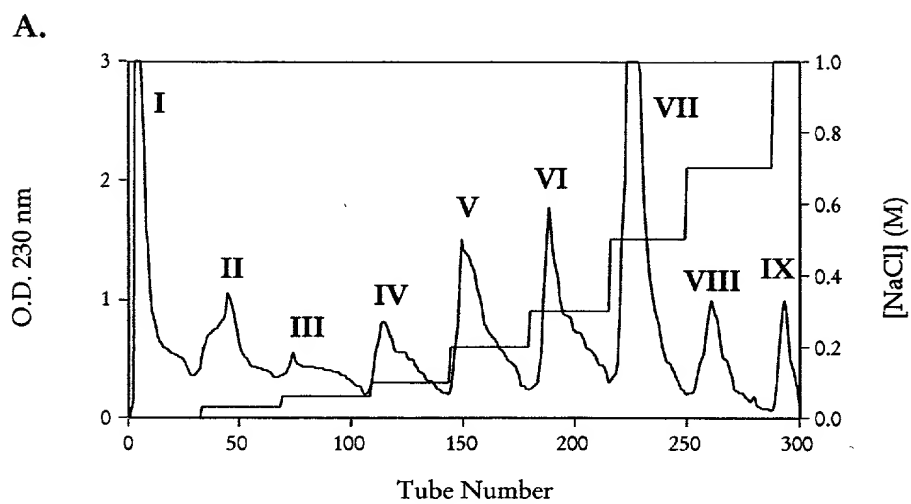


Fig. 1.1

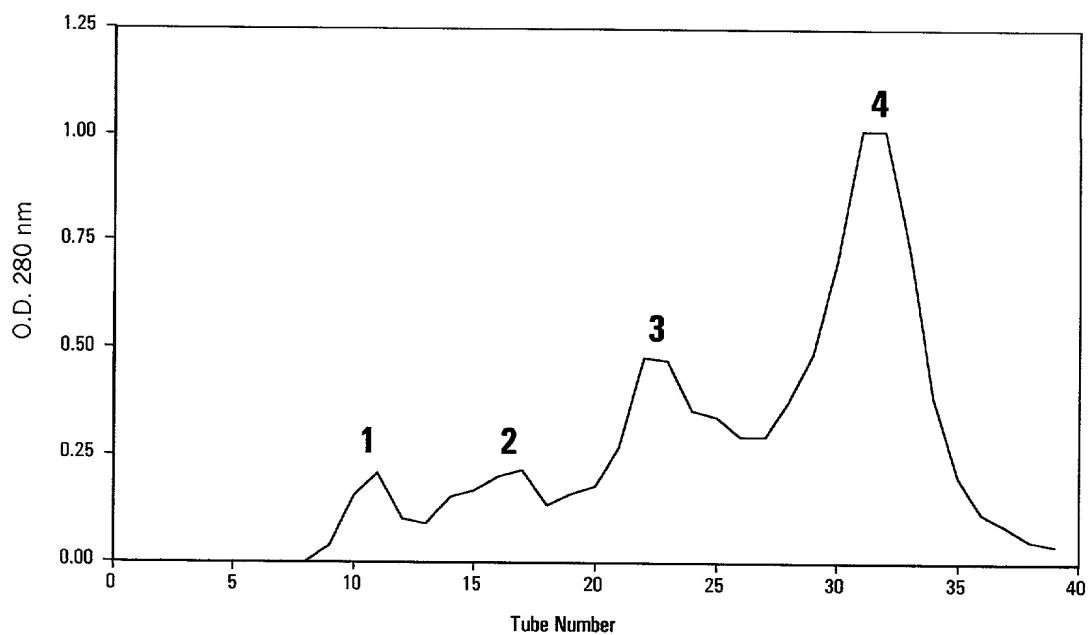


Fig. 1.2

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202210 84292860

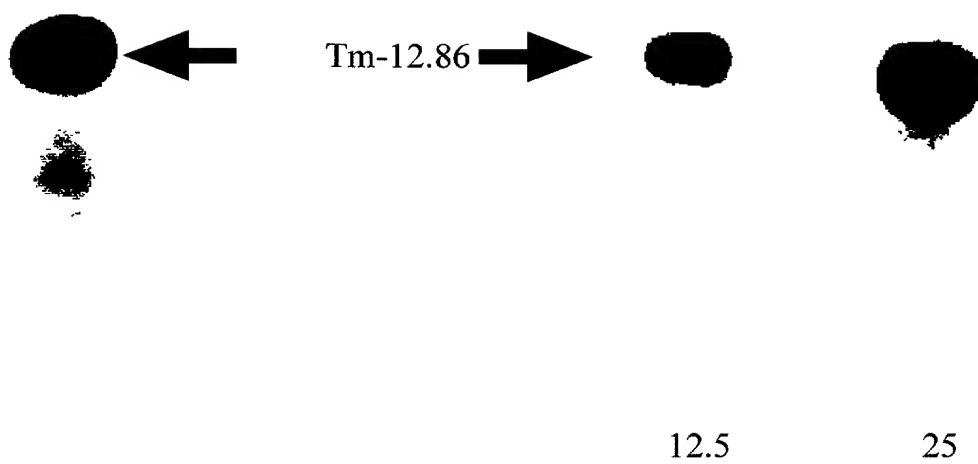


Fig. 1.3

Fig. 1.4

208210" 01:23:28.60

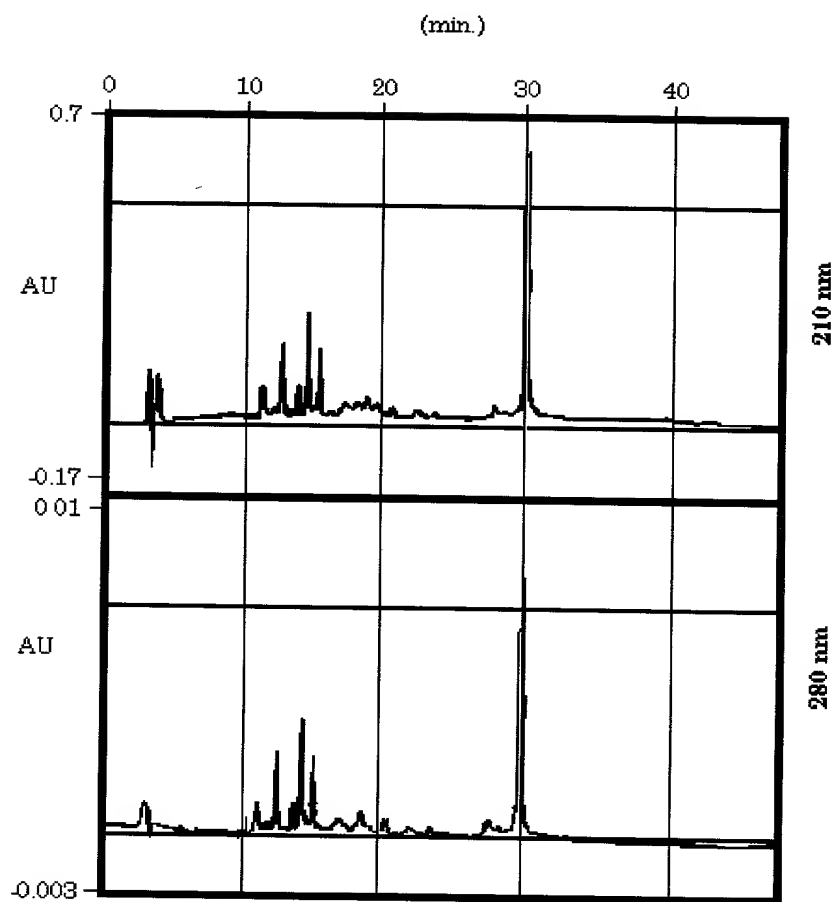


Fig. 1.5

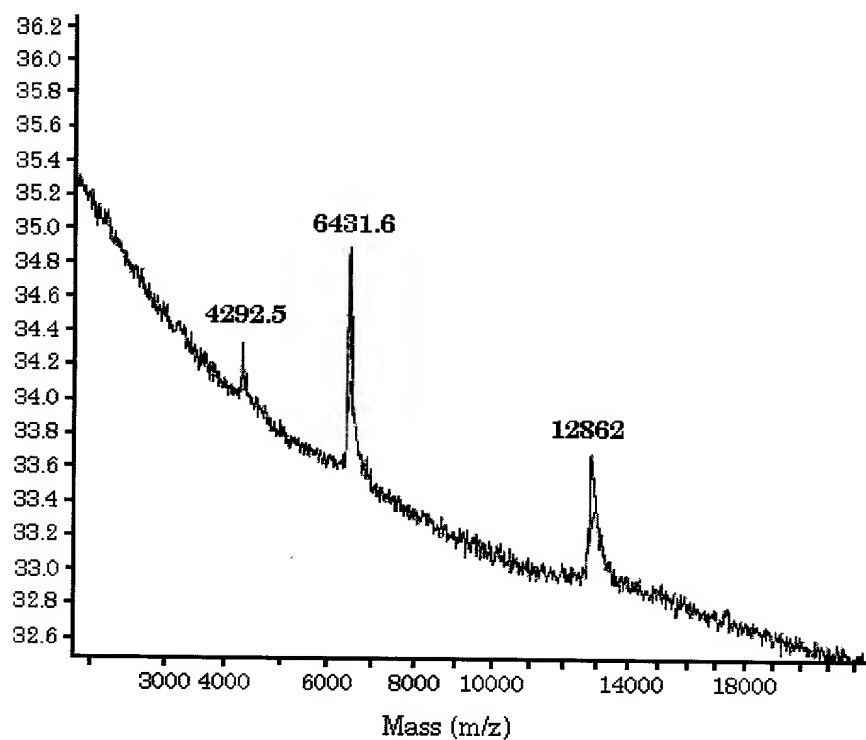


Fig. 1.6

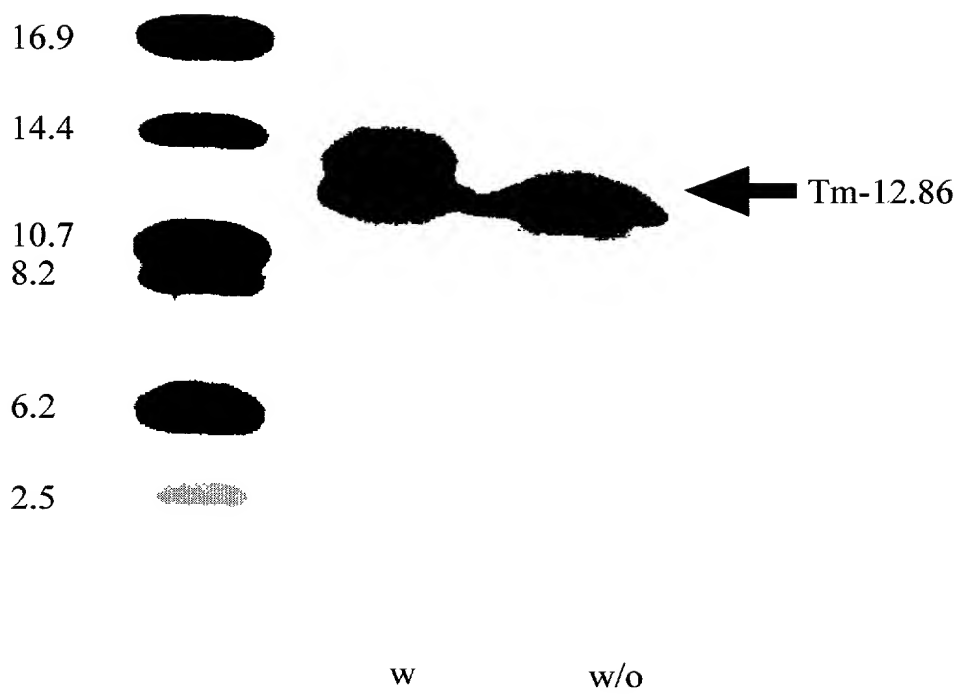


Fig. 1.7

NH_2 -L-T-D-E-Q-I-Q-K-R-N-K-I-S-K-E-?-Q-Q-V
 Val Gln Gln Glu Lys Ser Ile Lys Asn Arg Lys Gln Ile Gln Glu Asp Thr Leu

Fig. 1.8

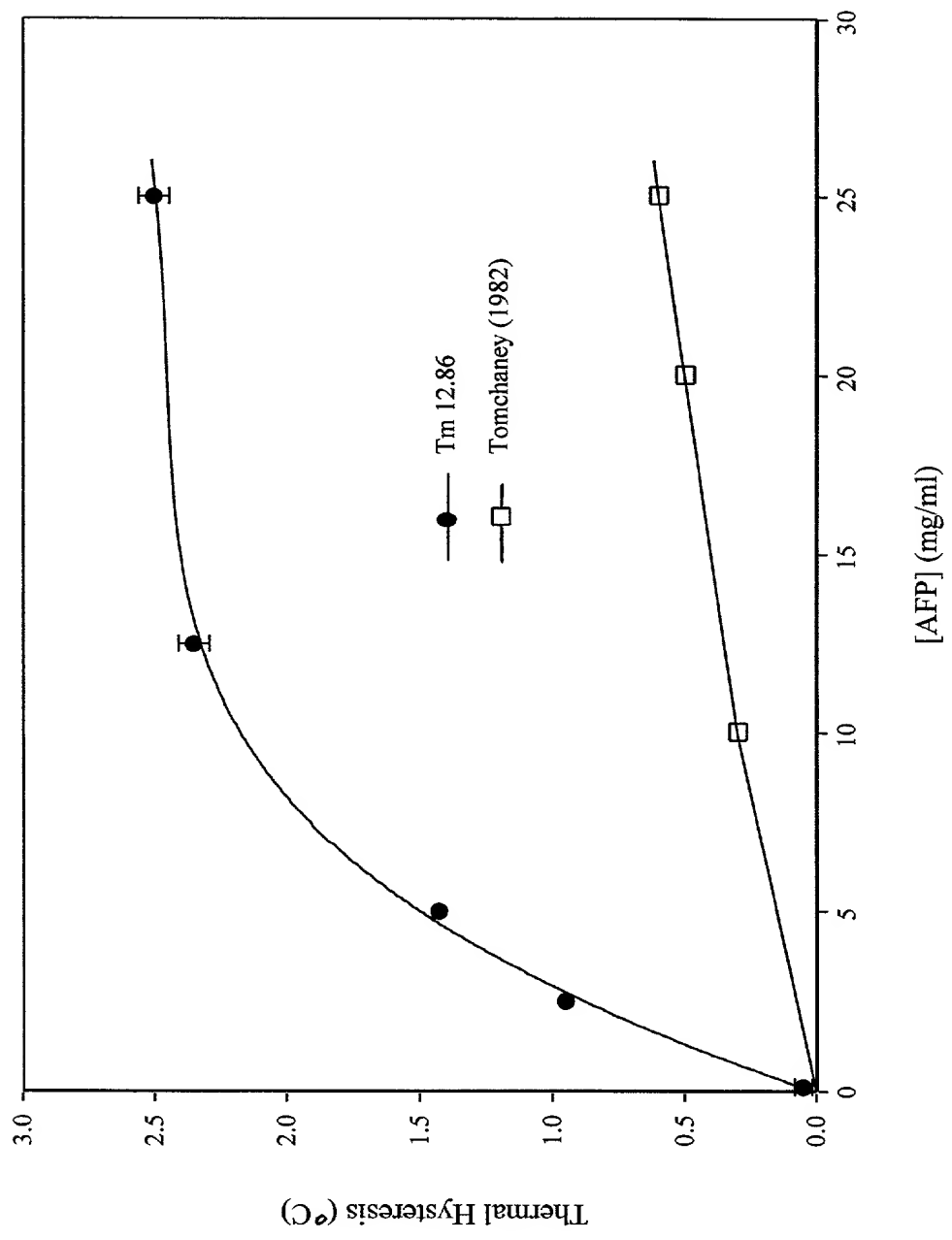


Fig. 1.9

09826348.012802

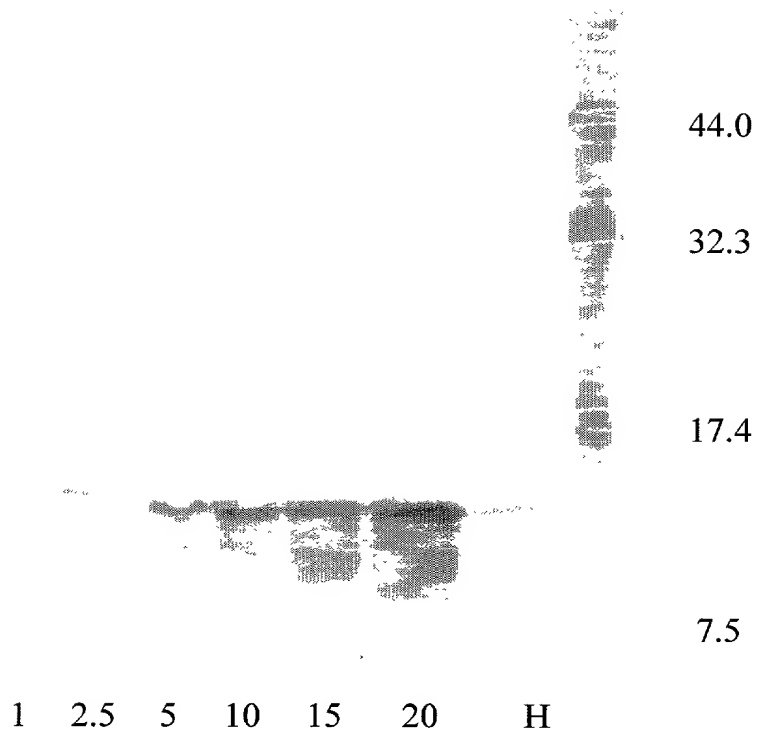


Fig. 1.10

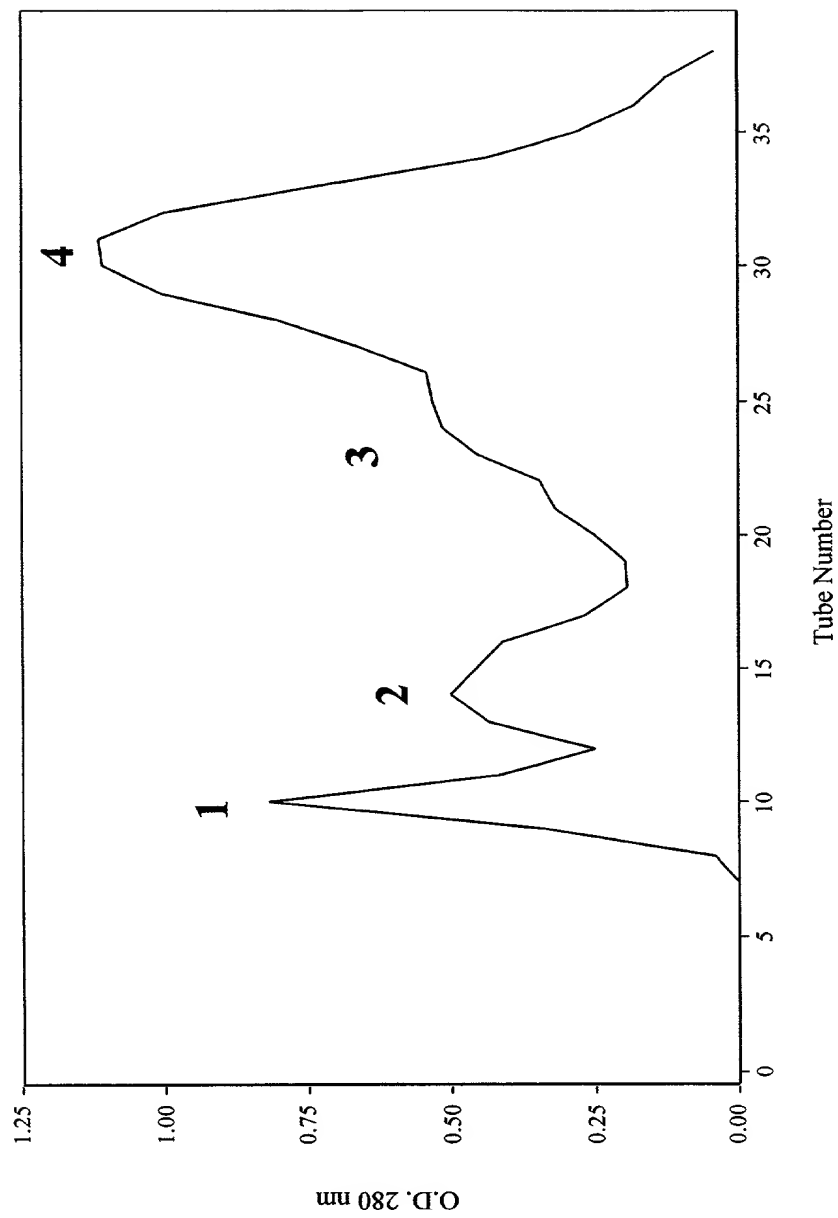


Fig. 1.11

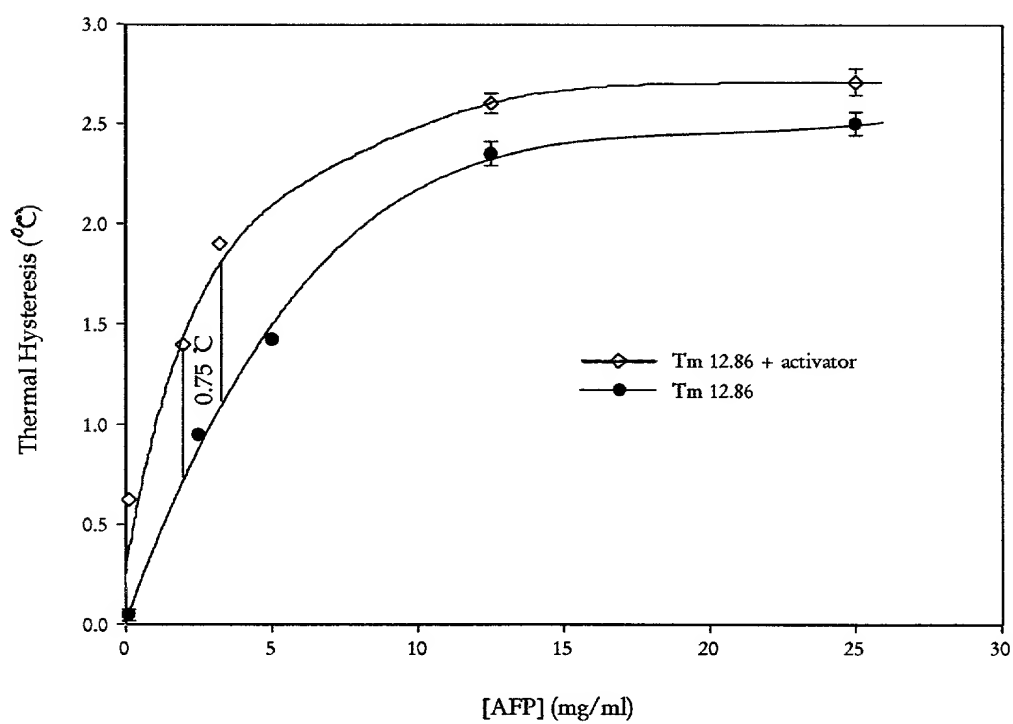


Fig. 1.12

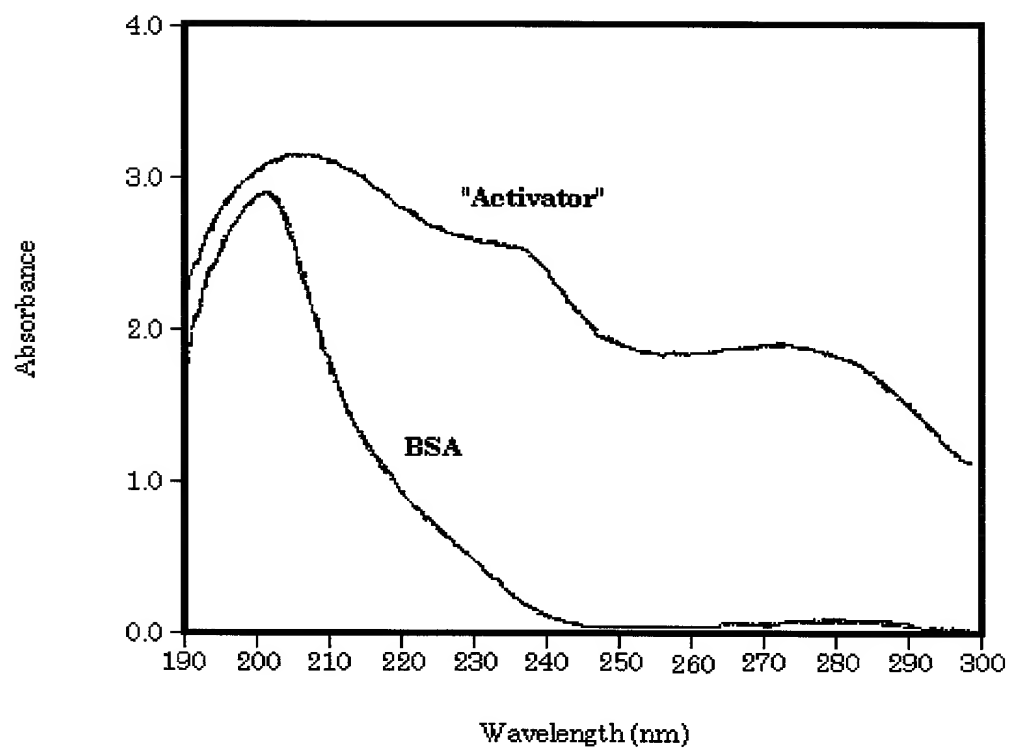


Fig. 1.13

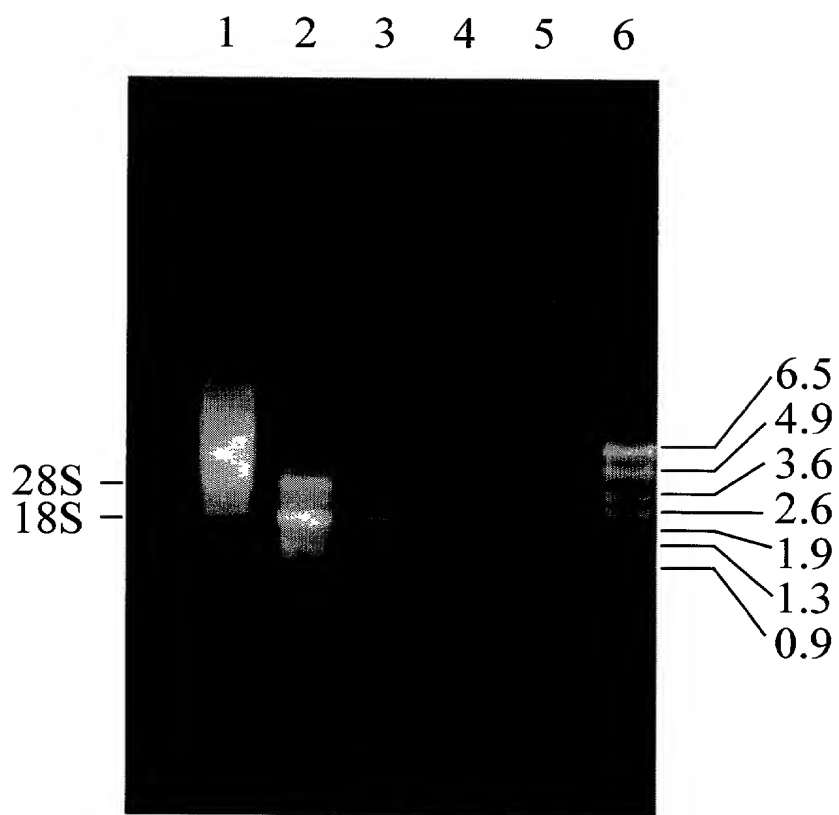


Fig. 2.0

202210-01E92B60

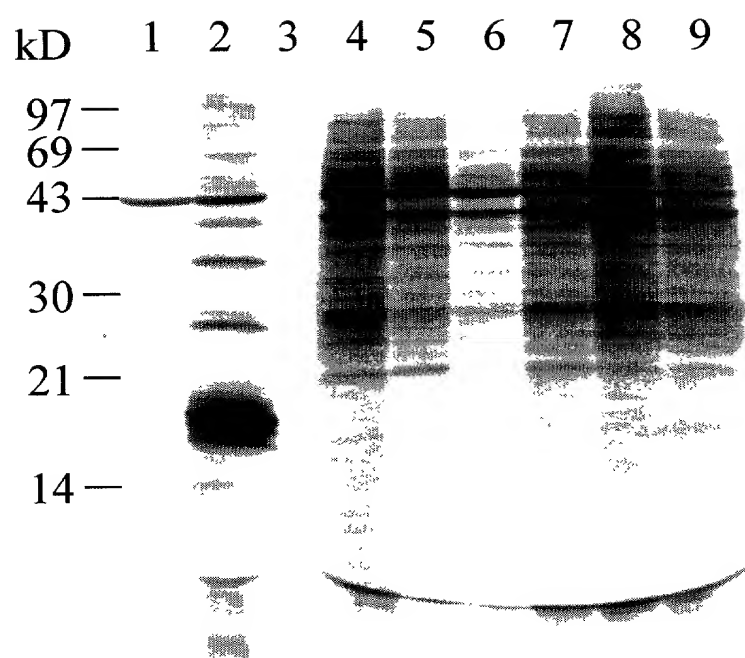


Fig. 2.1

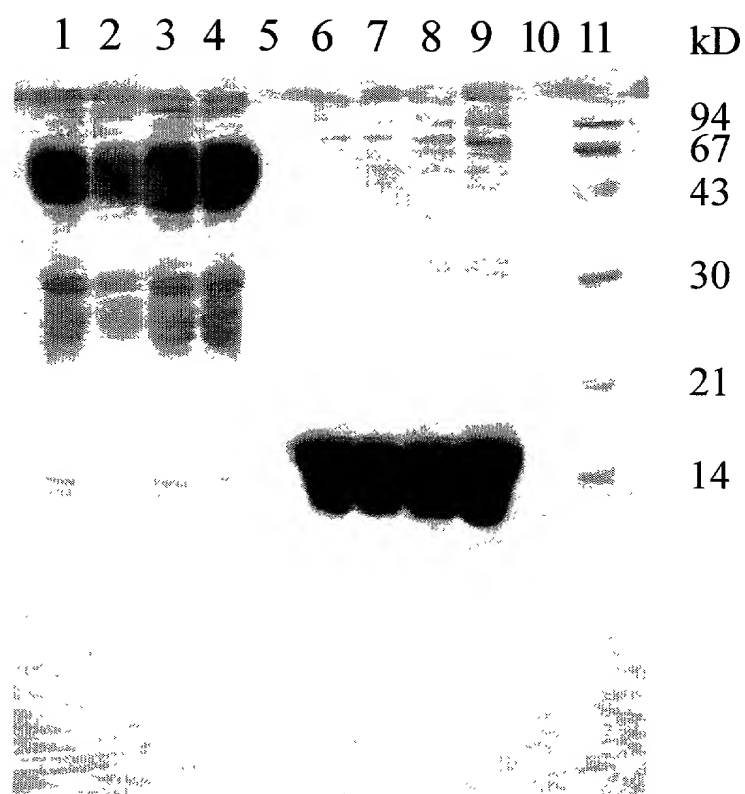


Fig. 2.2

09076348-012002

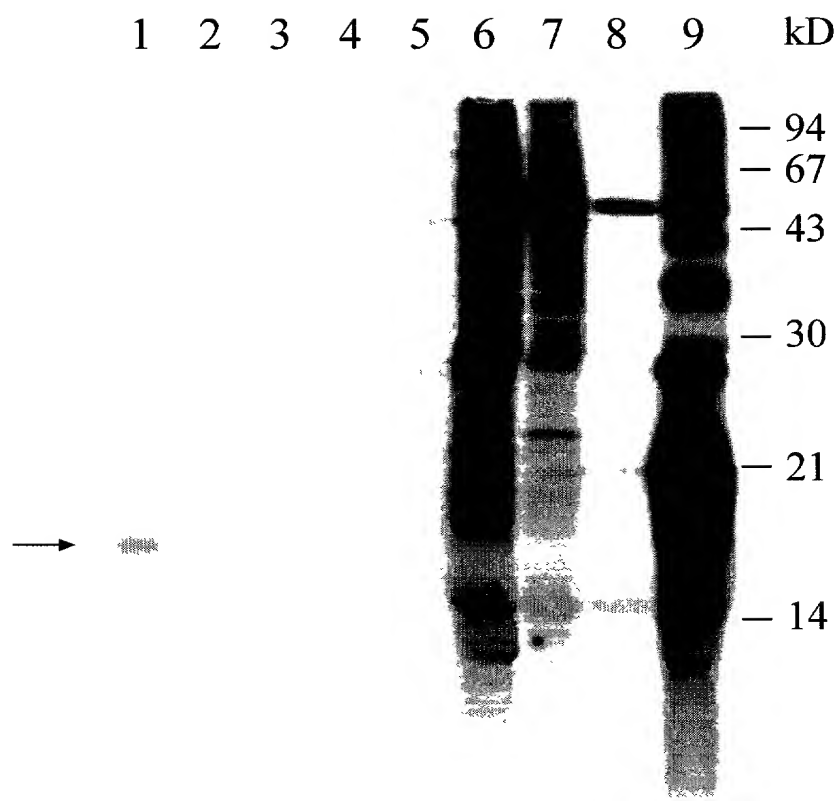


Fig. 2.3

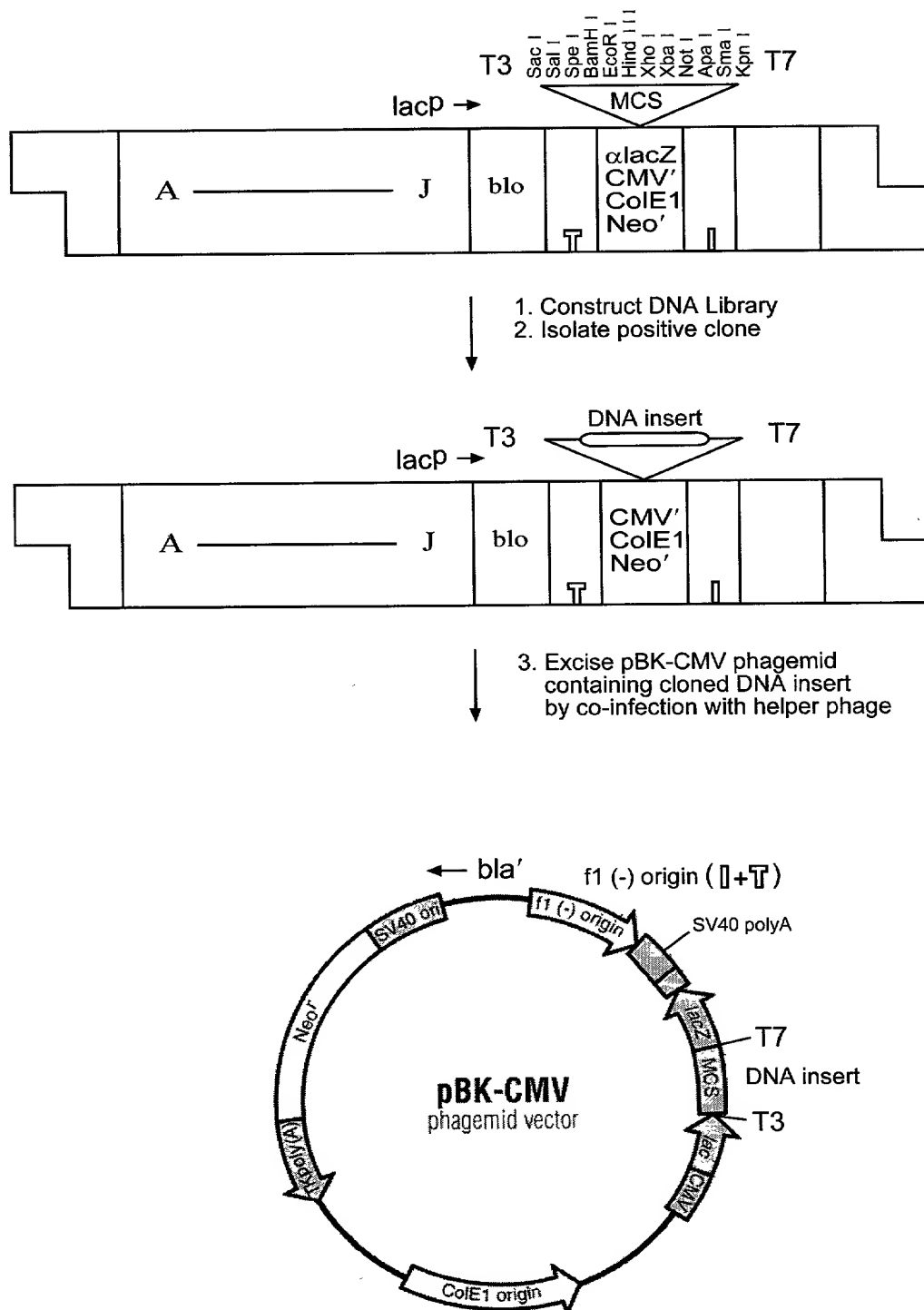


Fig. 2.4a

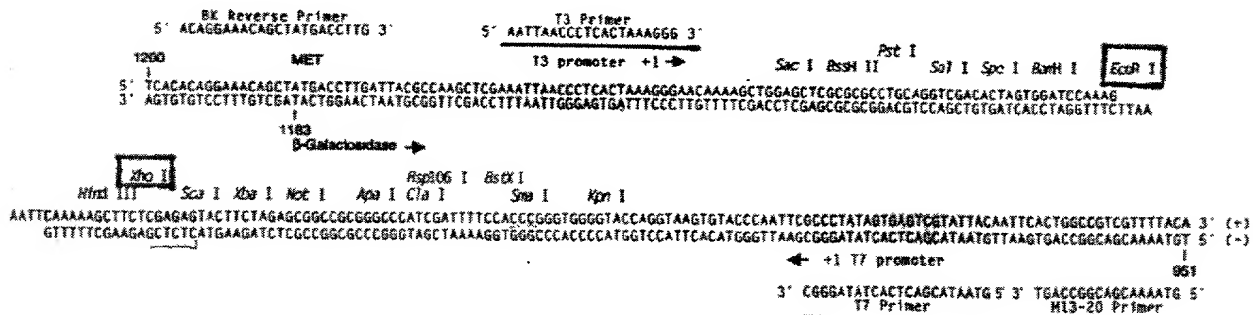
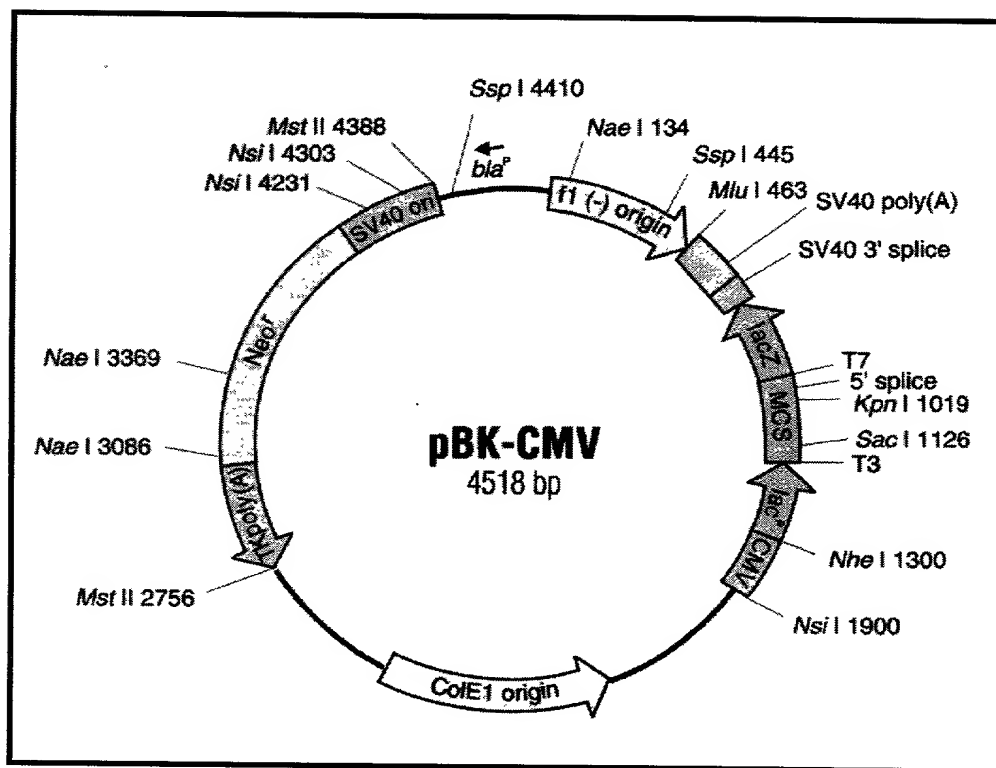


Fig 2.4b

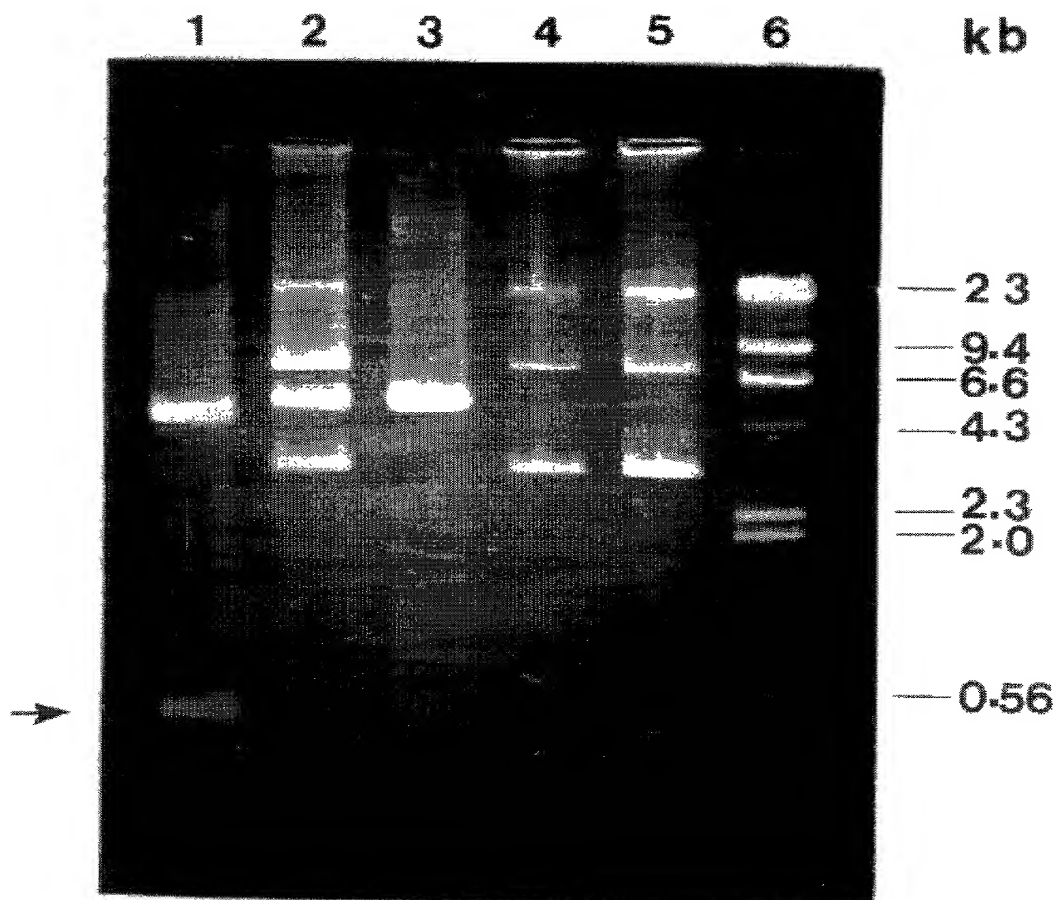


Fig. 2.5

DNA sequence of Tm 13.17 cDNA clone

B E
 a c
 m o
 H R
 I I

1 AGTGGATCCAAAGAATTCCGGCACGAGACTACTAAGATGAAGTTGCTCTGTTGTCTAATCT
 M K L L C C L I S

61 CCCTCATTCTGTTGGTCACAGTTCAGGCCCTGACCGAGGCACAAATTGAGAACTGAACA
 L I L L V T V Q A L T E A Q I E K L N K

121 AGATCAGCAAAAAATGTCAAAATGAAAGTGGAGTGTGCGCAAGAGATCATAACCAAAGCTC
 I S K K C Q N E S G V S Q E I I T K A R

181 GCAACGGTGAAGTGGGAGGACGATCCTAAACTGAAACGCCAAGTTTTTGGCGTGGCCAGGA
 N G D W E D D P K L K R Q V F C V A R N

241 ACGCCGGTCTGGCCACGGAATCGGGAGAGGTGGTGGTTCGACGTGTTGAGGGAGAAGGTGA
 A G L A T E S G E V V V D V L R E K V R

301 GGAAGGTCACTGACAACGACGAAGAAACTGAGAAAATCATCAATAAGTGCCTGTCGAAGA
 K V T D N D E E T E K I I N K C A V K R

361 GAGATACTGTTGAAGAGACGGTGTTCATACTTTCAAATGTGTCATGAAAAACAAGCCAA
 D T V E E T V F N T F K C V M K N K P K

421 AGTTCTCACCAGTTGATTGAACCACCACGACTAGTAGATGGTTCAAATGGTGTGCTTTAC
 F S P V D *

X
 h
 o
 I

481 ATATAAAATAAAGTGTCTCTGATGTAAAAAATAAAAAAAAAAAAAAAAAAACTCG
 polyadenylation signal poly (A) tail (26)

537 AGAGTATTCTAGAGCGGCCGCGGGCCCATCGTTTTCCACCC



Fig. 2.6b

A. Mature Tm 13.17 amino acid residue

1 LTEAQIEKLN KISKKCQNES GVSQEIIITKA RNGDWEDDPK LKRQVFCVAR
 51 NAGLATESGE VVVDVLREKV RKVTDNDEET EKIINKCAVK RDTVEETVFN
 101 TFKCVMKNKP KFSPVD

B. Summary of the composition analysis for the mature Tm 13.17 sequence:

<u>Residue</u>	<u>Number</u>	<u>Mole Percent</u>
A = Ala	6	5.172
B = Asx	0	0.000
C = Cys	4	3.448
D = Asp	8	6.897
E = Glu	13	11.207
F = Phe	4	3.448
G = Gly	4	3.448
H = His	0	0.000
I = Ile	6	5.172
K = Lys	16	13.793
L = Leu	5	4.310
M = Met	1	0.862
N = Asn	8	6.897
P = Pro	3	2.586
Q = Gln	4	3.448
R = Arg	6	5.172
S = Ser	5	4.310
T = Thr	8	6.897
V = Val	14	12.069
W = Trp	1	0.862
Y = Tyr	0	0.000
Z = Glx	0	0.000

Molecular weight = 13171.96; Residues = 116; Average Residue Weight = 113.551

Charge = 1; Isoelectric point = 7.74.

Fig. 2.6c

[illegible]

Fig. 2.7

Tm 13.17 3 EAQIEKLNKISKKQNESGVSQEIITKARNGDWEDDPKLKRQVFCVARNA 52
 |.. |||.. !. |..|||:| :..|| : ||||| :..||: :.
 AFP-3 1 ETPREKLKQHSDACKAESGVSEESLNKVRNREEVDDPKLKEHAFCLKRA 50

 Tm 13.17 53 GLATESGEVVVDVLRKVRKVTNDDEETEKIINKCAVKRDTVEETVFNTF 102
 |: ..|||. :| :..|.. :..{|...:..|||:|:|... : |
 AFP-3 51 GFIDASGEFQLDHIKTKFKENSEHPEKVDDLVAKCAVKKDTPOHSSADFF 100

 Tm 13.17 103 KCVMKNKP 110
 ||| .|:.
 AFP-3 101 KCVHDNRS 108

Percent identity: 39.8 (identical amino acids; Percent similarity: 58.3 (identical amino acids plus conservative amino acids).

Fig. 2.8

Tm 13.17	M	K	L	L	C	C	L	I	S	L	I	L	V	T	V	Q	A
AFP-3	M	K	L	L	L	C	L	V	L	V	A	L	V	A	T	Y	A
B Protein				L	T	S	L	I	L	L	V	A	V	Q	A		

Fig. 2.9

Tm 13.17	NH2-L T	E A	Q I	E	K L	N K I S K	K C	Q N E
		:	:	:				
Tm 12.86	NH2-L T	D E	Q I	Q	R	N K I S K E	? Q	Q V

Fig 2.10

09876543210

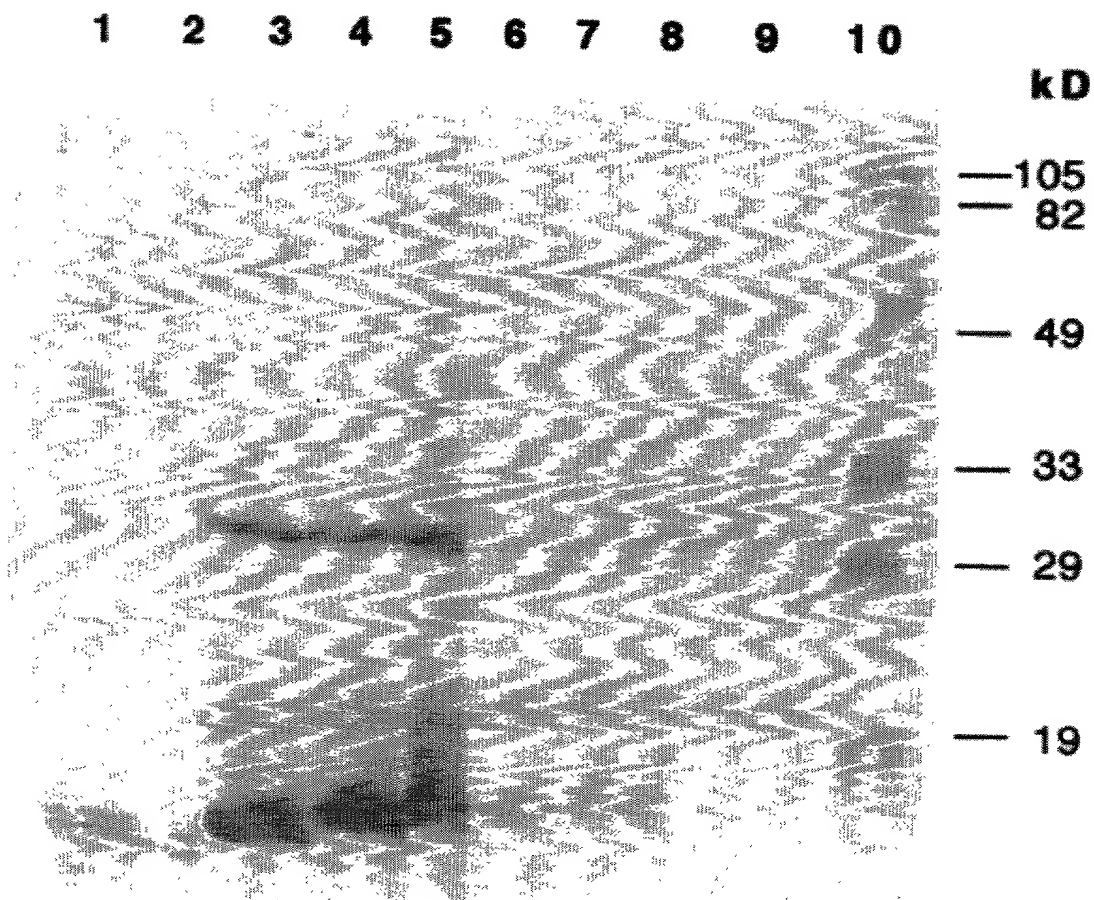


Fig 2.11

Tm 12.86 L T D E Q I Q K R N K I S K E ? Q Q V

Tm 13.17 1 L T E A Q I E K L N K I S K K C Q N E S G V S Q E I I T K A

B1 13 I T E E D L E L L R Q T S A E C K T E S G V S E D V I K R A

AFP-3 1 E T P R E K L K Q H S D A C K A E S G V S E E S L N K V

Tm13.17 31 R N G D W E D D P K L K R Q V F C V A R N A G L A T E S G E

B1 44 R K G D L E D D P K L K M Q L L C I F K A L E I V A E S G E

AFP-3 29 R N R E E V D D P K L K E H A F C I L K R A G F I D A S G E

Tm13.17 61 V V V D V L R E K V R K V T D N D E E T E K I I N K C A V K

B1 75 I E A D T F K E K L T R V T N D D E E S E K I V E K C T V T

AFP-3 59 F Q L D H I K T K F K E N S E H P E K V D D L V A K C A V K

Tm13.17 91 R D T V E E T V F N T F K C V M K N K P K F S P V D

B1 106 E D T P E D T A F E V T K C V L K D K P N F F G D L F V

AFP-3 89 K D T P Q H S S A D F F K C V H D N R S

Fig. 2.12

1 GGCACGAGCAAAA ATGAAACTCCTCTTGTGCTTTGCGTTTCGCCGCC
M K L L L C F A F A A

47 ATCGTCATCGGAGGCTCAGGCTCTCACCGACGAACAGATACAGAAA
I V I G A Q A L T D E Q I Q K

92 AGGAACAAGATCAGCAAAGAATGCCAGCAGGTGTCCGGAGTGTCC
R N K I S K E C Q Q V S G V S

137 CAAGAGACGATCGACAAAGTCCGCACAGGTGTCTTGGTCGATGAT
Q E T I D K V R T G V L V D D

182 CCCAAAATGAAGAAGCACGTCCTCTGCTTCTCGAAGAAAACTGGA
P K M K K H V L C F S K K T G

226 GTGGCAACCGAAGCCGGAGACACCAATGTGGAGGTACTCAAAGCC
V A T E A G D T N V E V L K A

271 AAGCTGAAGCATGTGGCCAGCGACGAAGAGGTGGACAAGATCGTG
K L K H V A S D E E V D K I V

316 CAGAAGTGCGTGGTCAAGAAGGCCACACCAGAGGAAACGGCTTAT
Q K C V V K K A T P E E T A Y

361 GACACCTTCAAGTGTATTTACGACAGCAAACCTGATTTCTCTCCT
D T F K C I Y D S K P D F S P

406 ATTGATTAATTGTTTTGTATTTGACTGAATTTTGACAATAAAGGT
I D

451 ACTATCGTTATGTAAAAAAAAAAAAAAAAAAAAA

polyadenylation signal

poly (A) tail

Fig. 3.0

polyadenylation signal

Fig 3.1

Start



2-2 GGCACGAGGCAAAAATGAAACTCCTCTTGTGCTTTGC[G]
 2-3 GGCACGAGGCAAAAATGAAACTCCTCTTGTGCTTTGCT

2-2 TTCGCCGCGCCATCGTCATCGGAGCTCAGGCTCTCACCG
 2-3 TTCGCCGCGCCATCGTCATCGGAGCTCAGGCTCTCACCG

2-2 ACGAACAGATACAGAAAAGGAACAAGATCAGCAAAGA
 2-3 ACGAACAGATACAGAAAAGGAACAAGATCAGCAAAGA

2-2 ATGCCAGCAGGTGTCCGGAGTGTCCCAAGAGACGATC
 2-3 ATGCCAGCAGGTGTCCGGAGTGTCCCAAGAGACGATC

2-2 GACAAAGTCCGCACAGGTGTCTTGGTCGAT[GATCCCA
 2-3 GACAAAGTCCGCACAGGTGTCTTGGTCGAC[GATCCCA

2-2 AAATGAAGAAAGCACGTCCTCTGCTTCTCGAAGAAAAC
 2-3 AAATGAAGAAAGCACGTCCTCTGCTTCTCGAAGAAAAC

2-2 TGGAGTGGCAACCGAAGCCGGAGACACCAATGTGGAG
 2-3 TGGAGTGGCAACCGAAGCCGGAGACACCAATGTGGAG

2-2 GTACTCAAAGCCAAGCTGAAGCATGTGGCCAGCGACG
 2-3 GTACTCAAAGCCAAGCTGAAGCATGTGGCCAGCGACG

2-2 AAGA[G]GTGGACAAGATCGTGCAGAAGTGCGTGGTCAA
 2-3 AAGA[A]GTGGACAAGATCGTGCAGAAGTGCGTGGTCAA

2-2 GAAGGCCACACCCAGAGGAAACGGCTTATGACACCTTC
 2-3 GAAGGCCACACCCAGAGGAAACGGCTTATGACACCTTC

2-2 AAGTGTATTTACGACAG[C]AAACCTGATTTCTCTCCTA
 2-3 AAGTGTATTTACGACAG[T]AAACCTGATTTCTCTCCTA

2-2 TTGATTAAATTGTTTTGTATTTGACTGAATTTTGACAA
 2-3 TTGATTAAATTGTTTTGTATTTGACTGAATTTTGACAA

2-2 TAAAGGTAT[A]TATCGTTATGT[A]AAAAA
 2-3 TAAAGGTAT[C]TATCGTTATGA[A]AAAAA

Fig 3.2

Predicted Amino Acid

Composition of 2-2 and 2-3

Analysis	Whole Protein
Molecular Weight	12843.80 m.w.
Length	115
1 microgram =	77.859 pMoles
Molar Extinction coefficient	3040±5%
1 A(280) =	4.22 mg/ml
Isoelectric Point	7.11
Charge at pH 7	0.13

Whole Protein Composition Analysis

Amino Acid(s)	Number count	% by weight	% by frequency
Charged (RKHYCDE)	48	47.19	41.74
Acidic (DE)	20	18.90	17.39
Basic (KR)	20	20.40	17.39
Polar (NCQSTY)	30	25.35	26.09
Hydrophobic (AILFWV)	34	27.26	29.57
A Ala	6	3.32	5.22
C Cys	4	3.21	3.48
D Asp	11	9.86	9.57
E Glu	9	9.05	7.83
F Phe	3	3.44	2.61
G Gly	4	1.78	3.48
H His	2	2.14	1.74
I Ile	6	5.29	5.22
K Lys	18	17.97	15.65
L Leu	5	4.41	4.35
M Met	1	1.02	0.87
N Asn	2	1.78	1.74
P Pro	4	3.02	3.48
Q Gln	6	5.98	5.22
R Arg	2	2.43	1.74
S Ser	7	4.75	6.09
T Thr	9	7.08	7.83
V Val	14	10.80	12.17
W Trp	0	0.00	0.00
Y Tyr	2	2.54	1.74
B Asx	0	0.00	0.00
Z Glx	0	0.00	0.00
X Xxx	0	0.00	0.00
. Ter	0	0.00	0.00

Fig. 3.3

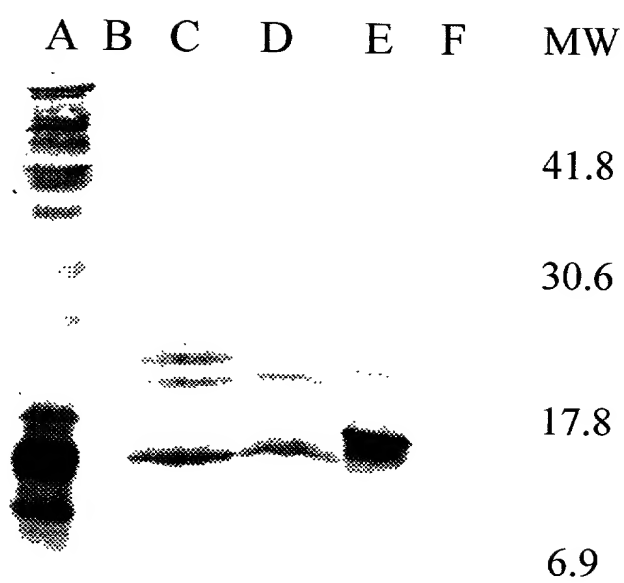


Fig. 3.4

Lane

1 2 3 4 5

a → 577 bp
b → 483 bp

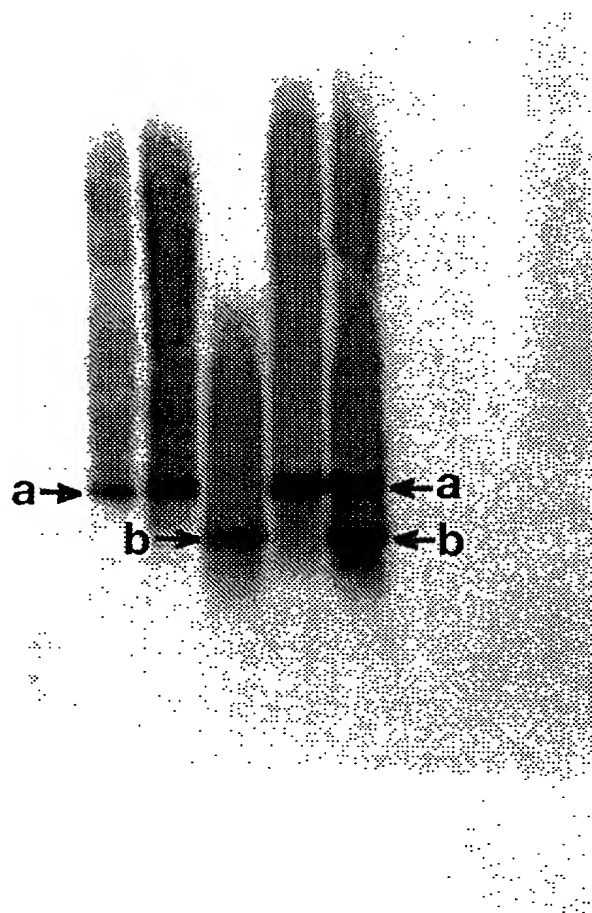


Fig. 4.0

208270.84E94860

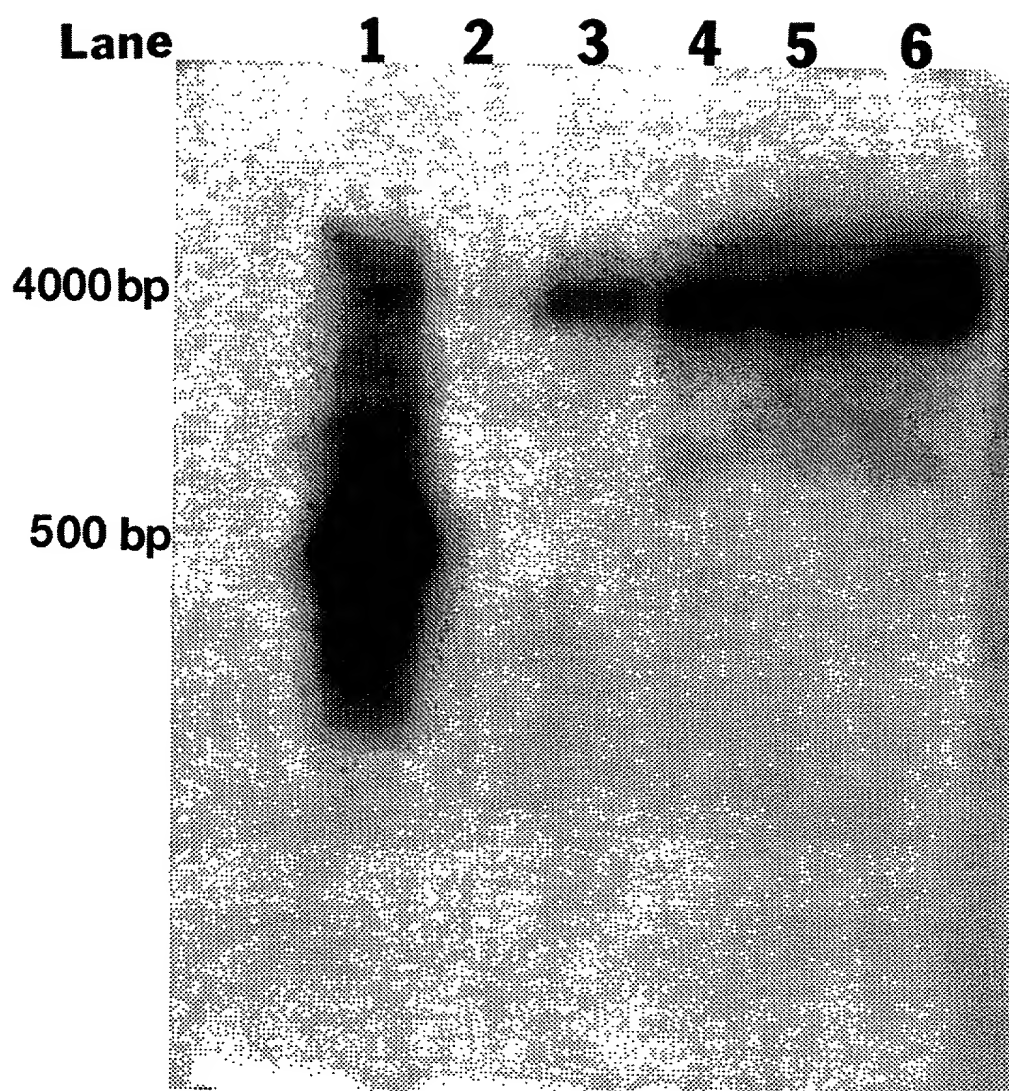


Fig. 4.1

20221018123000

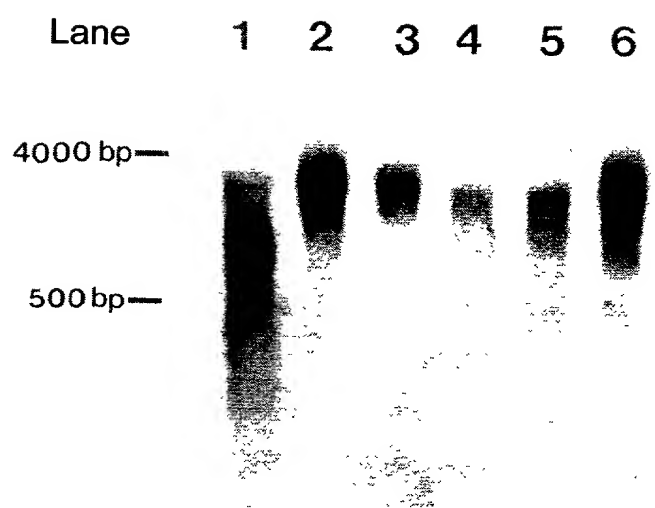
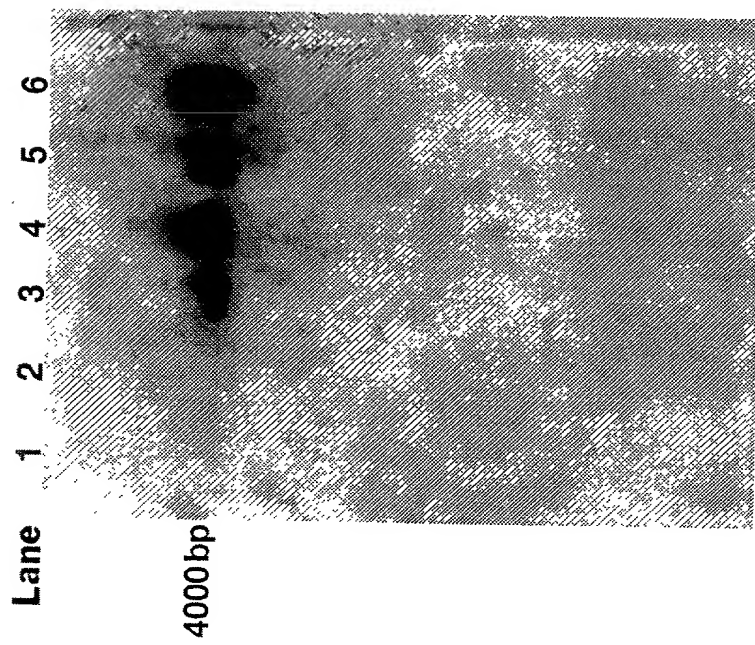


Fig. 4.2

A.



B.

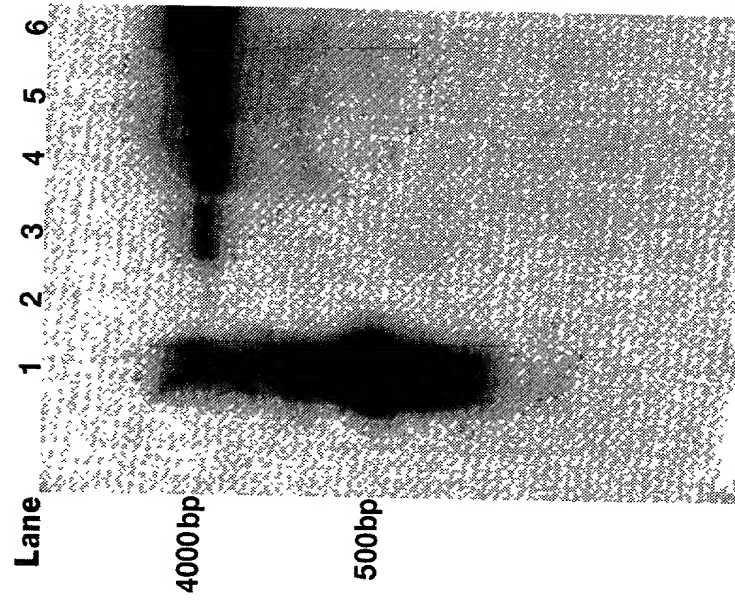


Fig. 4.3

20221018 01:23:49

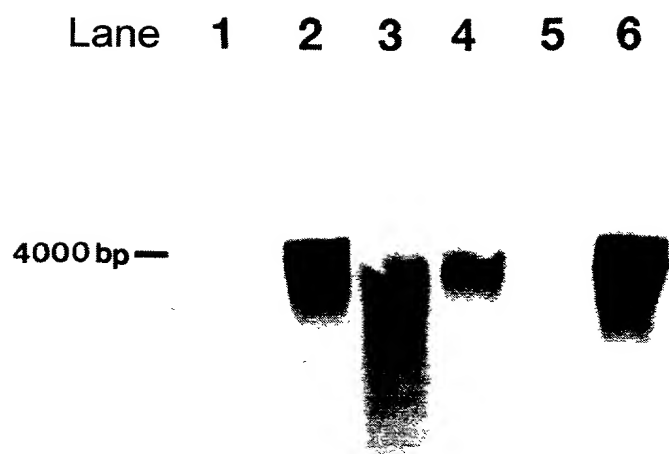


Fig. 4.4

208210 04E94060

Lane

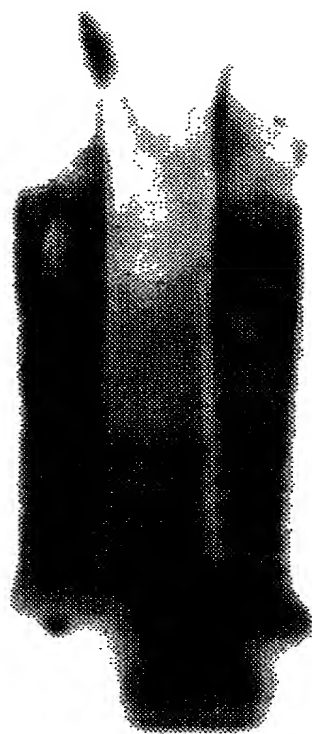
1

2

3

4

5



23130

9416

4361

2322

2027

564

Fig. 4.5

Tm 13.17 cDNA

1 AGTGGATCCAAAGAATTTCGGCACGAGACTACTAAGATGAAGTTGCTCTGTTGTCTAATCT
M K L L C C L I S

61 CCCTCATTCTGTTGGTTCACAGTTCAGGCCCTGACCGAGGCACAAATTGAGAACTGAACA
L I L L V T V Q A L T E A Q I E K L N K
↑ Forward Primer

121 AGATCAGCAAAAAATGTCAAAATGAAAGTGGAGTGTGCGCAAGAATGATCATAACCAAGCTC
I S K K C Q N E S G V S Q E I I T K A R

181 GCAACGGTGAAGTGGGAGGACGATCCTAAACTGAAACGCCAAGTTTTTTGCGTGGCCAGGA
N G D W E D D P K L K R Q V F C V A R N

241 ACGCCGGTCTGGCCACGGAATCGGGAGAGGTGGTGGTTCGACGTGTTGAGGGAGAAGGTGA
A G L A T E S G E V V V D V L R E K V R

301 GGAAGGTCACCTGACAACGACGAAGAACTGAGAAAATCATCAATAAGTGCGCCGTCAAGA
K V T D N D E E T E K I I N K C A V K R
Reverse Primer

361 GAGATACTGTTGAAGAGACGGTGTTCATACTTTCAAATGTGTTCATGAAAAACAAGCCAA
D T V E E T V F N T F K C V M K N K P K

421 AGTTCTCACCAGTTGATTGAACCACCACGACTAGTAGATGGTTCAAATGGTGTGCTTTAC
F S P V D *

481 ATATAAAATATAAGTGTTTCTGATGTAAAAAATAAAAAAAAAAAAAAAAAAACTCG
polyadenylation signal poly (A) tail (26)

537 AGAGTATTCTAGAGCGGCCGCGGGCCCATCGTTTTCCACCC

Fig. 4.6a

Forward Primer

2-2 LTDEQIQKRNKISKECQQVS **GVSQE** TIDKVRTGVLV
Tm 13.17 LTEAQIEKLNKISKKCQNES **GVSQE** IITKARNGDWE
B2 LTEEDLQLLRQTSAECKTES **GASEA** VIKKARKGDLE
AFP-3 ETPREKLKQHS DACKAES **GVSEE** SLNKVRNREEV

2-2 DDPKMKKHVLCFSKKTGVATEAGDTNVEVLKAKLKH
Tm 13.17 DDPKLKRQVFCVARNAGLATESGEVVVDVLRKVRK
B2 DDPKLKMQLLCIFKALEIVAESGEIEADTFKEKLTR
AFP-3 DDPKLKEHAFICILKRAGFIDASGEFQLDHIKTKFKE

Reverse Primer

2-2 VAS DEEVDKIVQKCVVKK **ATPEET** AYDTFKCIYDS
Tm 13.17 VTDNDEETEKIINKCAVKR **DTVEET** VFNTFKCVMKN
B2 VTNDDEESEKI VEKCTVTE **DTPEDT** AFEVTKCVLKD
AFP-3 NSEHPEKVDDLVAKCAVKK **DT PQHS** SADFFKCVHDN

2-2 KPDFSPI D
Tm 13.17 KPKFSPVD
B2 KPNFFGDLFV
AFP-3 RS

Fig. 4.6b

Primer	percent % composition				MeltingTemperature(°C)
	A	C	G	T	
Forward	28.6	14.3	42.9	14.3	44.0
Reverse	25.0	31.3	6.3	37.5	44.0

Fig. 4.6c

09076348.012802

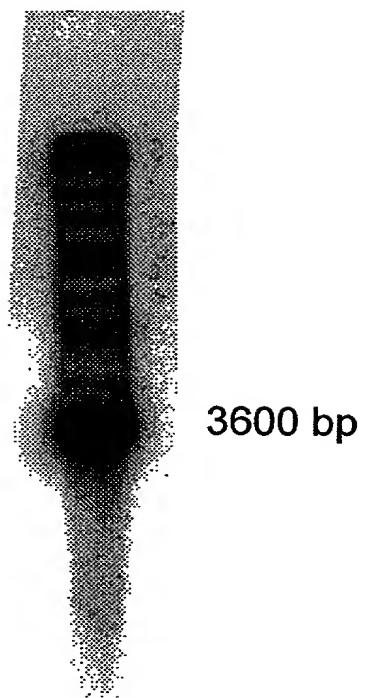


Fig. 4.7

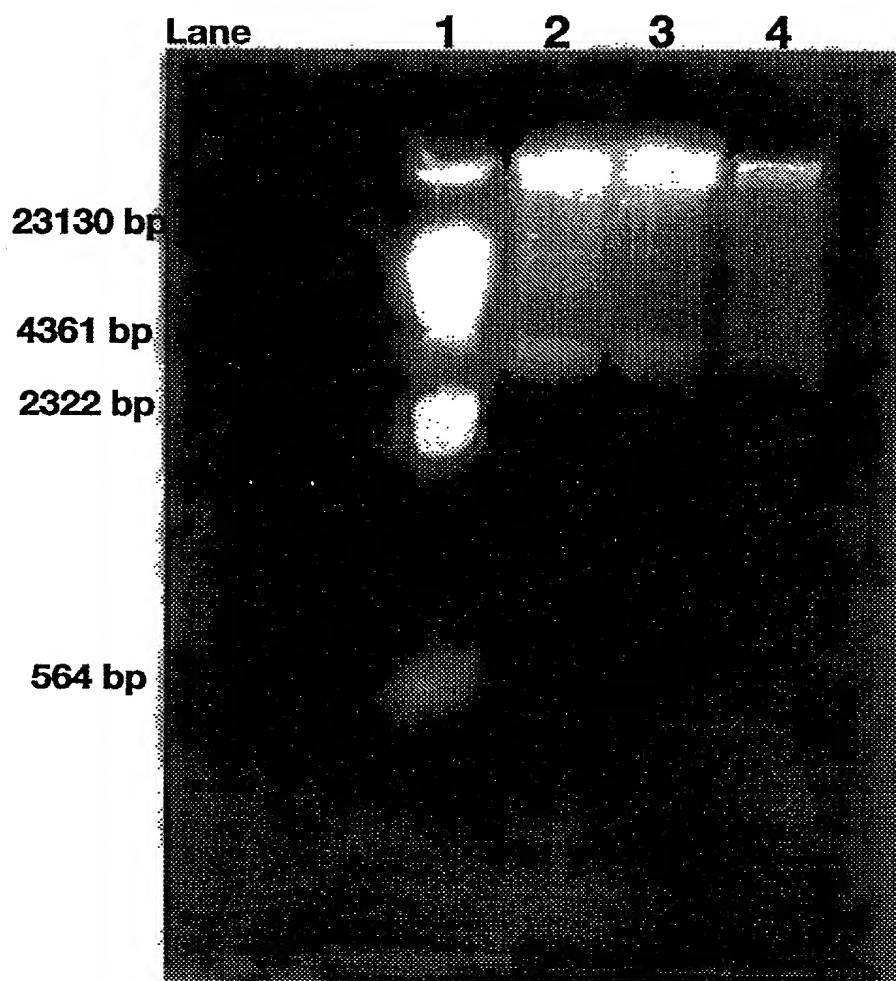


Fig. 4.8

208270-BHE9/860

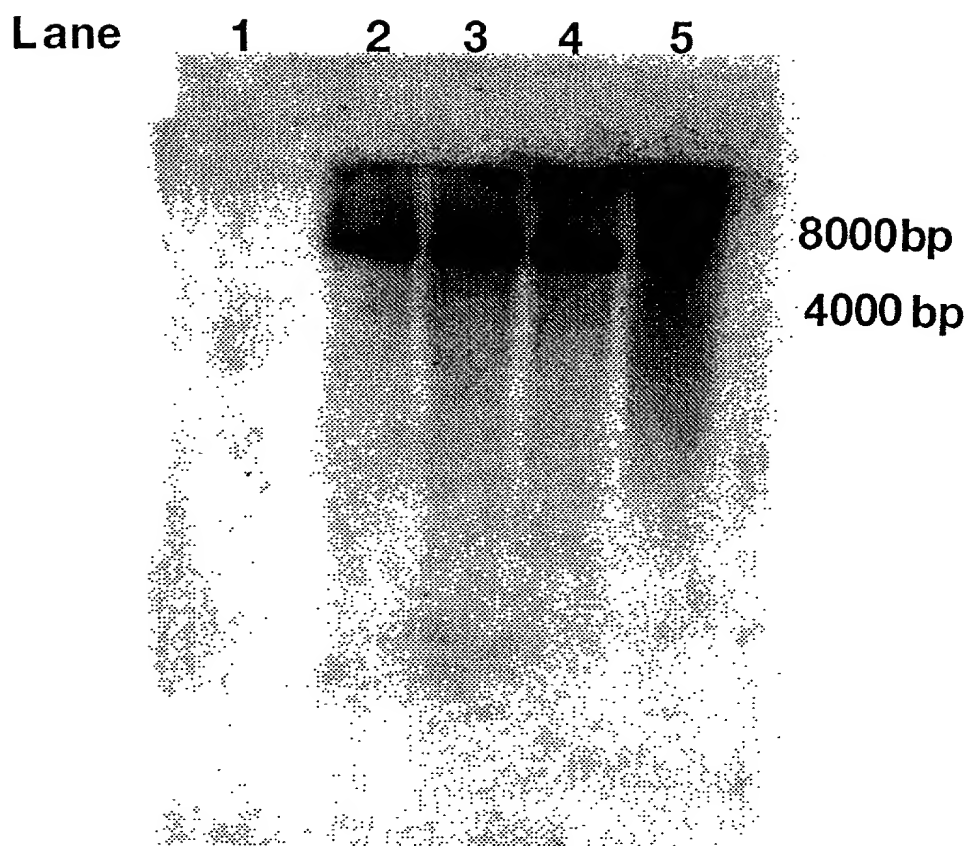


Fig. 4.9

1 GGCACGAGCAAAA ATGAAACTCCTCTTGTGCTTTGCTTTGCGCGCC
M K L L L C F A F A A

47 ATCGTCATCGGAGCTCAGGCTCTCACCGACGAACAGATACAGAAA
I V I G A Q A L T D E Q I Q K

92 AGGAACAAGATCAGCAAAGAATGCCAGCAGGTGTCCGGAGTGTCC
R N K I S K E C Q Q V S G V S

137 CAAGAGACGATCGACAAAGTCCGCACAGGTGTCTTGGTCGACGAT
Q E T I D K V R T G V L V D D

182 CCCAAAATGAAGAAGCACGTCCTCTGCTTCTCGAAGAAAACCTGGA
P K M K K H V L C F S K K T G

226 GTGGCAACCGAAGCCGGAGACACCAATGTGGAGGTACTCAAAGCC
V A T E A G D T N V E V L K A

271 AAGCTGAAGCATGTGGCCAGCGACGAAGAGGTGGACAAGATCGTG
K L K H V A S D E E V D K I V

316 CAGAAGTGCGTGGTCAAGAAGGCCACACCAGAGGAAACGGCTTAT
Q K C V V K K A T P E E T A Y

361 GACACCTTCAAGGTTATTTACGACAGTAAACCTGATTTCTCTCCT
D T F K V I Y D S K P D F S P

406 ATTGATTAATTGTTTTGTATTTGACTGAATTTTGACAATAAAGGT
I D *

451 ACTATCGTTATGTAAAAAAAAAAAAAAAAAAAAA polyadenylation signal

poly (A) tail

Fig. 4.10a

Predicted Amino Acid

Composition of 3-4

Molecular Weight	12839.70 m.w.
Length	115
1 microgram =	77.883 pMoles
Molar Extinction coefficient	2920±5%
1 A(280) =	4.40 mg/ml
Isoelectric Point	7.14
Charge at pH 7	0.16

Whole Protein Composition Analysis

Amino Acid(s)	Number count	% by weight	% by frequency
Charged (RKHYCDE)	47	46.41	40.87
Acidic (DE)	20	18.91	17.39
Basic (KR)	20	20.41	17.39
Polar (NCQSTY)	29	24.55	25.22
Hydrophobic (AILFWV)	35	28.04	30.43
A Ala	6	3.32	5.22
C Cys	3	2.41	2.61
D Asp	11	9.86	9.57
E Glu	9	9.05	7.83
F Phe	3	3.44	2.61
G Gly	4	1.78	3.48
H His	2	2.14	1.74
I Ile	6	5.29	5.22
K Lys	18	17.97	15.65
L Leu	5	4.41	4.35
M Met	1	1.02	0.87
N Asn	2	1.78	1.74
P Pro	4	3.02	3.48
Q Gln	6	5.99	5.22
R Arg	2	2.43	1.74
S Ser	7	4.75	6.09
T Thr	9	7.09	7.83
V Val	15	11.58	13.04
W Trp	0	0.00	0.00
Y Tyr	2	2.54	1.74
B Asx	0	0.00	0.00
Z Glx	0	0.00	0.00
X Xxx	0	0.00	0.00
. Ter	0	0.00	0.00

Fig. 4.10b

1 GGCACGAGCAAAA ATGAAACTCCTCTTGTGCTTTGCTTTGCGCCGCC
M K L L L C F A F A A

47 ATCGTCATCGGAGCTCAGGCTCTCACCGATGAACAGATACAGAAA
I V I G A Q A L T D E Q I Q K

92 AGGAACAAGATCAGCAAAGAATGCCAGCAGGAGTCCGGAGTGTCC
R N K I S K E C Q Q E S G V S

137 CAAGAGACGATCGACAAAGTCCGCACAGGTGTCTTGGTCGACGAT
Q E T I D K V R T G V L V D D

182 CCCAAAATGAAGAAGCACGTCCTCTGCTTCTCGAAGAGAACTGGA
P K M K K H V L C F S K R T G

226 GTGGCAACCGAAGCCGGAGACACCAATGTGGAGGTACTCAAAGCC
V A T E A G D T N V E V L K A

271 AAGCTGAAGCATGTGGCCAGCGACGAAGAAGTGGACAAGATCGTG
K L K H V A S D E E V D K I V

316 CAGAAGTGCGTGGTCAAGAAGGCCACACCAGAGGAAACGGCTTAT
Q K C V V K K A T P E E T A Y

361 GACACCTTCAAGTGTATTTACGACAGTAAACCTGATTTCTCTCCT
D T F K V I Y D S K P D F S P

406 ATTGATTAAATTGTTTTGTATTTGACTGAATTTTGACAATAAAGGT
I D * **polyadenylation signal**

451 ACTATCGTTATGAAAAAAAAAAAAAAAAAAAA

poly (A) tail

Fig. 4.11a

Predicted Amino Acid

Composition of 3-9

Analysis	Whole Protein
Molecular Weight	12871.80 m.w.
Length	115
1 microgram =	77.689 pMoles
Molar Extinction coefficient	3040±5%
1 A(280) =	4.23 mg/ml
Isoelectric Point	7.11
Charge at pH 7	0.13

Whole Protein Composition Analysis

Amino Acid(s)	Number count	% by weight	% by frequency
Charged (RKHYCDE)	48	47.31	41.74
Acidic (DE)	20	18.86	17.39
Basic (KR)	20	20.57	17.39
Polar (NCQSTY)	30	25.29	26.09
Hydrophobic (AILFWV)	34	27.20	29.57
A Ala	6	3.31	5.22
C Cys	4	3.21	3.48
D Asp	11	9.84	9.57
E Glu	9	9.03	7.83
F Phe	3	3.43	2.61
G Gly	4	1.77	3.48
H His	2	2.13	1.74
I Ile	6	5.28	5.22
K Lys	17	16.93	14.78
L Leu	5	4.40	4.35
M Met	1	1.02	0.87
N Asn	2	1.77	1.74
P Pro	4	3.02	3.48
Q Gln	6	5.97	5.22
R Arg	3	3.64	2.61
S Ser	7	4.74	6.09
T Thr	9	7.07	7.83
V Val	14	10.78	12.17
W Trp	0	0.00	0.00
Y Tyr	2	2.54	1.74
B Asx	0	0.00	0.00
Z Glx	0	0.00	0.00
X Xxx	0	0.00	0.00
. Ter	0	0.00	0.00

Fig. 4.11b

1 GGCACGAGCAAAA ATG AAACTCCTCTTGTGCTTTGCGTTGCGCGCC
M K L L L C F A F A A

47 ATCGTCATCGGAGCTCAGGCTCTCACCGACGAACAGATACAGAAA
I V I G A Q A L T D E Q I Q K

92 AGGAACAAGATCAGCAAAGAGTGCCAGCAGGTGTCCGGAGTGTCC
R N K I S K E C Q Q E S G V S

137 CAAGAGACGATCGACAAAGTCCGCACAGGTGTCTTGGTCGACGAT
Q E T I D K V R T G V L V D D

182 CCCAAAATGAAGAAGCACGTCCTCTGCTTCTCGAAGAAAACCTGGA
P K M K K H V L C F S K R T G

226 GTGGCAACCGAAGCCGGAGACACCAATGTGGAGGTA CTCAAAGCC
V A T E A G D T N V E V L K A

271 AAGCTGAAGCATGTGGCCAGCGACGAAGAAGTGGACAAGATCGTG
K L K H V A S D E E V D K I V

316 CAGAAGTGCGTGGTCAAGAAGGCCACACCAGAGGAAACGGCTTAT
Q K C V V K K A T P E E T A Y

361 GACACCTTCAAGTGTATTTACGACAGTAAACCTGATTTCTCTCCT
D T F K V I Y D S K P D F S P

406 ATTGATTAAATTGTTTTGTATTTGGCTGAATTTTGACAATAAAGGT
I D

451 ACTATCGTTATGTAAAAAAAAAAAAAAAAAAAAA

polyadenylation signal

poly (A) tail

Fig. 4.12a

Predicted Amino Acid

Composition of 7-5

Analysis	Whole Protein
Molecular Weight	12843.80 m.w.
Length	115
1 microgram =	77.859 pMoles
Molar Extinction coefficient	3040±5%
1 A(280) =	4.22 mg/ml
Isoelectric Point	7.11
Charge at pH 7	0.13

Whole Protein Composition Analysis

Amino Acid(s)	Number count	% by weight	% by frequency
Charged (RKHYCDE)	48	47.19	41.74
Acidic (DE)	20	18.90	17.39
Basic (KR)	20	20.40	17.39
Polar (NCQSTY)	30	25.35	26.09
Hydrophobic (AILFWV)	34	27.26	29.57
A Ala	6	3.32	5.22
C Cys	4	3.21	3.48
D Asp	11	9.86	9.57
E Glu	9	9.05	7.83
F Phe	3	3.44	2.61
G Gly	4	1.78	3.48
H His	2	2.14	1.74
I Ile	6	5.29	5.22
K Lys	18	17.97	15.65
L Leu	5	4.41	4.35
M Met	1	1.02	0.87
N Asn	2	1.78	1.74
P Pro	4	3.02	3.48
Q Gln	6	5.98	5.22
R Arg	2	2.43	1.74
S Ser	7	4.75	6.09
T Thr	9	7.08	7.83
V Val	14	10.80	12.17
W Trp	0	0.00	0.00
Y Tyr	2	2.54	1.74
B Asx	0	0.00	0.00
Z Glx	0	0.00	0.00
X Xxx	0	0.00	0.00
. Ter	0	0.00	0.00

Fig. 4.12b

2-2	↓	MKLL	LCFA	FAFA	AAI	VI	GACQ	ALT	TDEQ	QKRN	KI	SKEC	CCQ	QVSS	GGV	SSQ	ETI	DKV	VRT	GGV	LV
2-3		MKLL	LCFA	FAFA	AAI	VI	GACQ	ALT	TDEQ	QKRN	KI	SKEC	CCQ	QVSS	GGV	SSQ	ETI	DKV	VRT	GGV	LV
3-4		MKLL	LCFA	FAFA	AAI	VI	GACQ	ALT	TDEQ	QKRN	KI	SKEC	CCQ	QVSS	GGV	SSQ	ETI	DKV	VRT	GGV	LV
3-9		MKLL	LCFA	FAFA	AAI	VI	GACQ	ALT	TDEQ	QKRN	KI	SKEC	CCQ	QVSS	GGV	SSQ	ETI	DKV	VRT	GGV	LV
7-5		MKLL	LCFA	FAFA	AAI	VI	GACQ	ALT	TDEQ	QKRN	KI	SKEC	CCQ	QVSS	GGV	SSQ	ETI	DKV	VRT	GGV	LV
2-2		DDPK	MMKK	HHV	LCF	SFK	KTG	VAT	TEAG	DTN	VEV	LKAK	LLK	HVVA	SS	DEE	VVD	KI	VQK	CCV	VKK
2-3		DDPK	MMKK	HHV	LCF	SFK	KTG	VAT	TEAG	DTN	VEV	LKAK	LLK	HVVA	SS	DEE	VVD	KI	VQK	CCV	VKK
3-4		DDPK	MMKK	HHV	LCF	SFK	KTG	VAT	TEAG	DTN	VEV	LKAK	LLK	HVVA	SS	DEE	VVD	KI	VQK	CCV	VKK
3-9		DDPK	MMKK	HHV	LCF	SFK	KTG	VAT	TEAG	DTN	VEV	LKAK	LLK	HVVA	SS	DEE	VVD	KI	VQK	CCV	VKK
7-5		DDPK	MMKK	HHV	LCF	SFK	KTG	VAT	TEAG	DTN	VEV	LKAK	LLK	HVVA	SS	DEE	VVD	KI	VQK	CCV	VKK
2-2		ATPE	EET	AYD	TFK	CI	YDS	KPD	DFS	PI	D*										
2-3		ATPE	EET	AYD	TFK	CI	YDS	KPD	DFS	PI	D*										
3-4		ATPE	EET	AYD	TFK	CI	YDS	KPD	DFS	PI	D*										
3-9		ATPE	EET	AYD	TFK	CI	YDS	KPD	DFS	PI	D*										
7-5		ATPE	EET	AYD	TFK	CI	YDS	KPD	DFS	PI	D*										

	MW	AA	Cys	Pro	Phe	Ile	Val	Met	Leu	% most hydrophobic	(% mole)										% most hydrophilic	
	(kDa)	(#)									Gly	Ala	Tyr	His	Trp	Asx	Glx	Arg	Lys	Ser	Thr	
Tm 12.86	12.86	117	3.2	3.0	3.4	4.4	8.5	2.0	4.4	28.9	3.1	3.9	3.8	3.2	ND	10.7	15.0	3.6	14.9	6.8	6.3	57.3
Tm 13.17	13.17	116	3.13	2.21	4.47	5.16	10.5	1.0	4.3	29.11	1.73	3.24	0	0	1.41	0	0	7.12	15.6	3.31	6.14	32.14
2-2	12.84	115	3.21	3.02	3.44	5.29	10.8	1.02	4.41	27.26	1.78	3.32	2.54	2.14	0	0	0	2.43	18.0	4.75	7.08	32.23
2-3	12.84	115	3.21	3.02	3.44	5.29	10.8	1.02	4.41	27.26	1.78	3.32	2.54	2.14	0	0	0	2.43	18.0	4.75	7.08	32.23
3-4	12.84	115	2.41	3.02	3.44	5.29	11.6	1.02	4.41	28.04	1.78	3.32	2.54	2.14	0	0	0	2.43	18.0	4.75	7.09	32.24
3-9	12.87	115	3.21	3.02	3.43	5.28	10.8	1.02	4.40	27.20	1.77	3.31	2.54	2.13	0	0	0	3.64	16.9	4.74	7.07	32.38
7-5	12.84	115	3.21	3.02	3.44	5.29	10.8	1.02	4.41	27.26	1.78	3.32	2.54	2.14	0	0	0	2.43	18.0	4.75	7.08	32.23

Fig. 4.15

 = conserved cysteine (yellow); Boxed = conserved residues in Genes (red)

Tm 13.17

212

B7 prot

82 prot

Phn Antaa

activity - do

Pop_Mans

Upper Main:

Obj2_Man:

Pbpos-E-Df

Pbpos-F Dr

Pharmacokinetics of Dro

Pharmacology - 2010

Item 13.17

2-2

7-7
09 and

Sold 19

82 prot

Pbp_Antpo

Pbp_Manus

Obituary

Obp2 **Map**

[illegible]

10-3-2013

Popo-t - Dr

Dr. L. D. D. D.

Pbprp2_Dro

1317

1111

7.7

100 prot

B2 prot.

Pbb Antpo

Measure Wans

Obat Maw

Obn2 Min

2000

Phosphorus

Popos. - U

February 1997

Pbprq2_Dro

Fig. 4.17

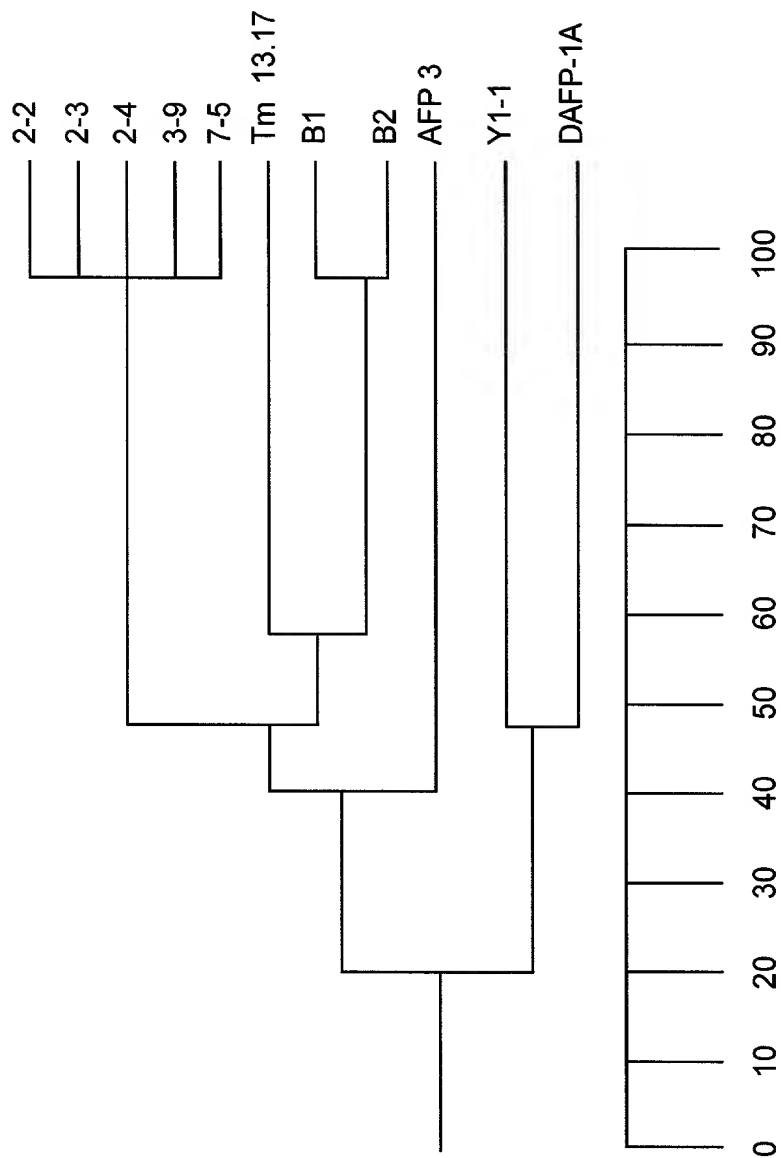
NUCLEOTIDE SEQUENCES

		PERCENT SIMILARITY											
		1 ²⁻²	2 ²⁻³	3 ³⁻⁴	4 ³⁻⁹	5 ⁷⁻⁵	6 ^{Tm13.17}	7 ^{B1}	8 ^{AFP-3}	9 ^{YL-1}	10 ^{DAFP-1A}		
PERCENT DIVERGENCE	1		99.1	97.3	98.4	98.2	50.4	42	42.4	20.7	20.9	1	2-2
	2	0.9		99	99	99	51.5	43.2	42.7	20.2	21.3	2	2-3
	3	1.6	60		98	98	50.3	42	42.1	20	20	3	3-4
	4	1.6	20	80		98.4	51.3	43.7	43.6	20.4	22	4	3-9
	5	1.8	25	75	45		50.4	42.5	42.9	22.2	23.1	5	7-5
	6	36.9	36.4	37.2	36.4	37.1		57.2	37.4	23.3	21	6	Tm 13.17
	7	39.9	41.2	41.7	40.7	41.2	30.2		39.3	21.9	22.1	7	B1
	8	41.8	42.4	43.1	42.3	42.3	45.3	49.4		21.8	23.1	8	AFP-3
	9	48.7	58.6	52	51.2	51.9	61.7	62.2	58.2		45.6	9	YL-1
	10	51.4	62.7	46.4	46.5	46.5	60	58.1	61.8	35.5		10	DAFP-1A
		1	2	3	4	5	6	7	8	9	10		

AMINO ACID SEQUENCES

		PERCENT SIMILARITY											
		1 ²⁻²	2 ²⁻³	3 ³⁻⁴	4 ³⁻⁹	5 ⁷⁻⁵	6 ^{Tm13.17}	7 ^{B1}	8 ^{AFP-3}	9 ^{YL-1}	10 ^{DAFP-1A}		
PERCENT DIVERGENCE	1		100	99.1	99.1	100	51.3	37.4	35.2	11.6	12	1	2-2
	2	0		99.1	99.1	100	51.3	37.4	35.2	11.6	12	2	2-3
	3	0.9	0.9		98.3	99.1	50.4	36.5	34.3	11.6	12	3	3-4
	4	0.9	0.9	1.7		99.1	51.3	37.4	36.1	10.7	12	4	3-9
	5	0	0	0.9	0.09		51.3	37.4	35.2	11.6	12	5	7-5
	6	46.1	46.1	47	46.1	46.1		47.4	39.8	13.4	13.9	6	Tm 13.17
	7	59.1	59.1	60	59.1	59.1	51.7		37	11.6	11.1	7	B1
	8	61.7	61.7	62.6	60.7	61.7	60.2	63		10.2	8.3	8	AFP-3
	9	86.7	86.7	85.7	85.7	85.7	86.8	84.2	87.5		55.6	9	YL-1
	10	88.3	88.3	86.4	84.5	85.4	89.1	82.7	90.5	40.2		10	DAFP-1A
		1	2	3	4	5	6	7	8	9	10		

Fig. 4.19



% Nucleic Acid Identity

Fig. 4.20

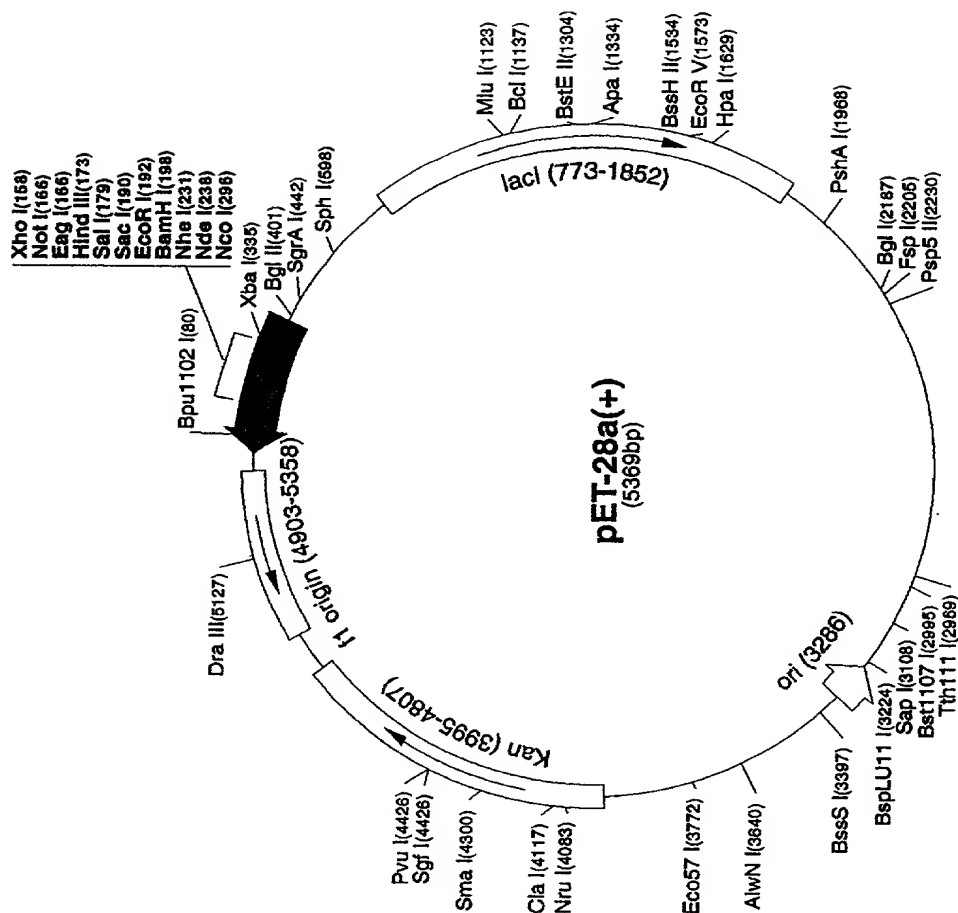


Fig. 5.0

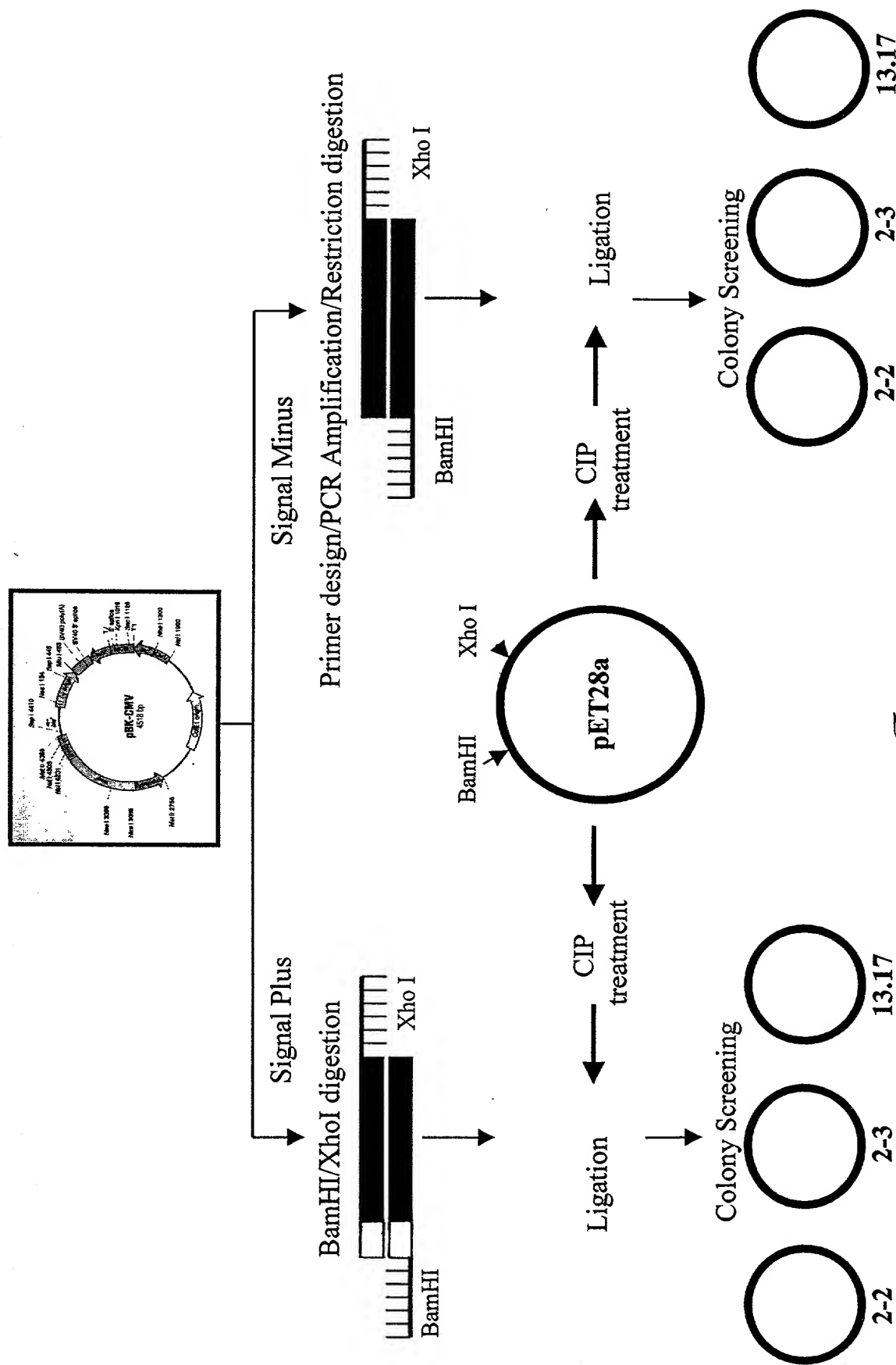


Fig. 5.1

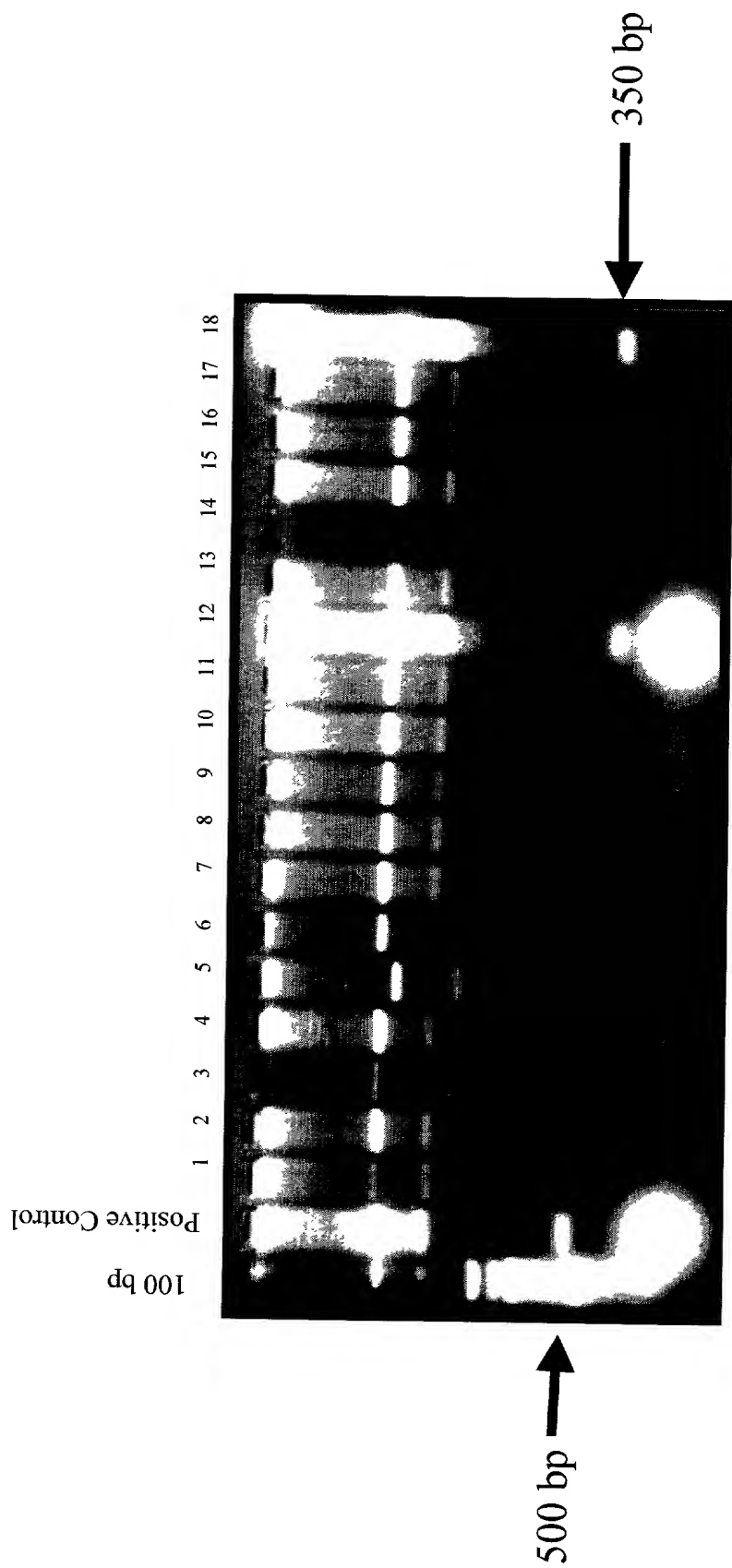


Fig. 5.2

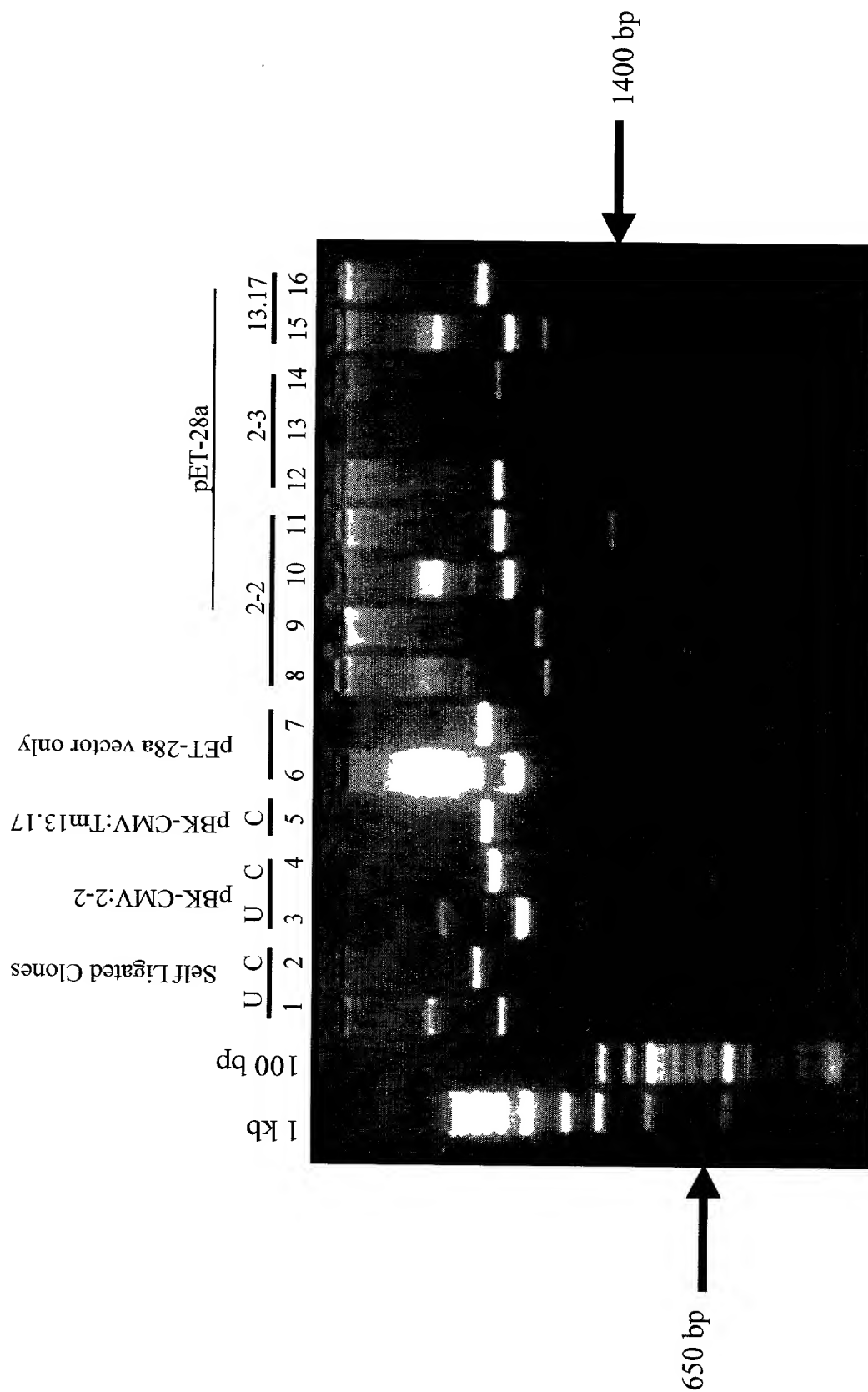


Fig. 5.3

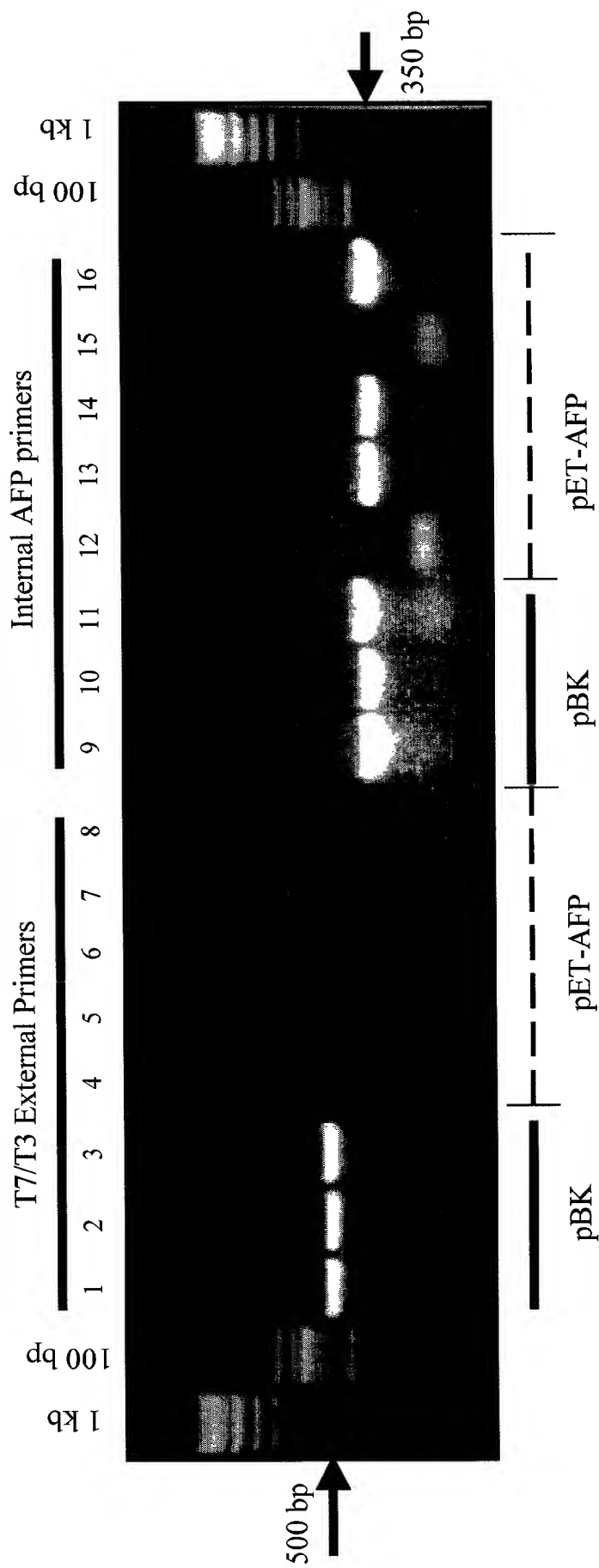


Fig. 5.4

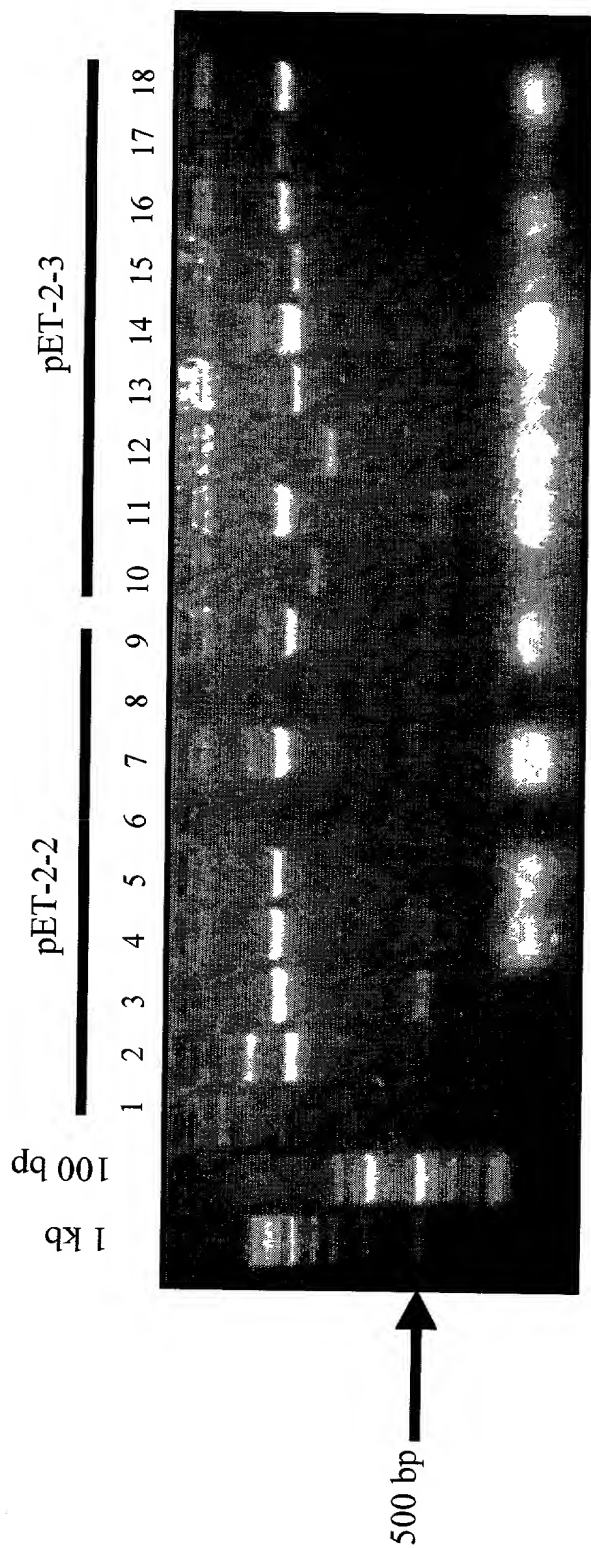


Fig. 5.5

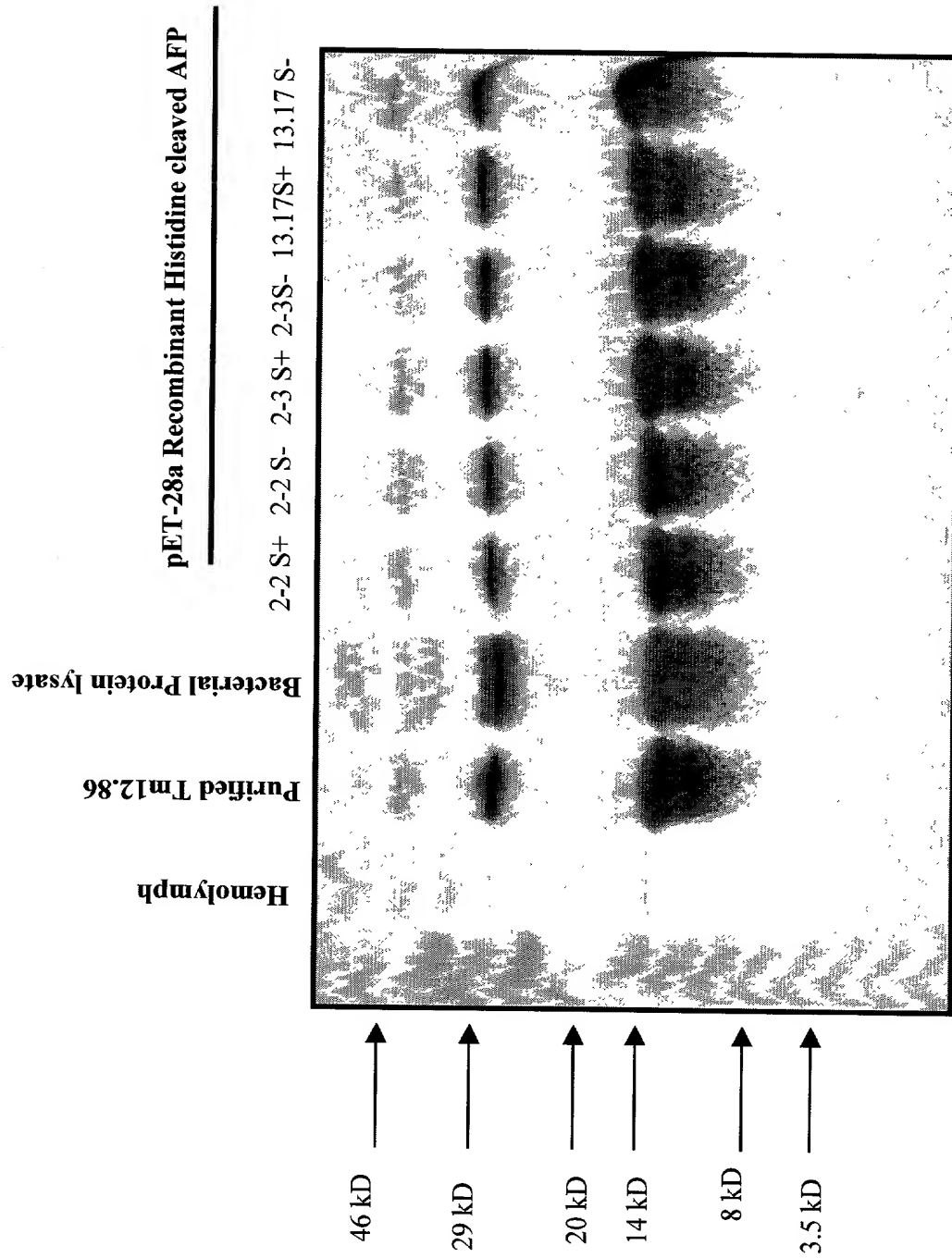


Fig 5.6

His-tagged Clone 2.2 with signal sequence

TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTA	50
His-tag Start Codon	
AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAC AGC	96
Met Gly Ser Ser His His His His His His Ser	
-55 -50	
AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT	141
Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly	
-45 -40 -35	
AFP Start Codon	
GGA CAG CAA ATG GGT CGC GGA TCC GAA TTC GCA CGA GCA AAA ATG	186
Gly Gln Gln Met Gly Arg Gly Ser Glu Phe Ala Arg Ala Lys Met	
-30 -25 -20	
AAA CTC CTC TTG TGC TTT GCG TTC GCC GCC ATC GTC ATC GGA GCT	231
Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala Ile Val Ile Gly Ala	
-15 -10 -5	
N-terminal of mature AFP	
CAG GCT CTC ACC GAC GAA CAG ATA CAG AAA AGG AAC AAG ATC AGC	276
Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser	
1 5 10	
AAA GAA TGC CAG CAG GTG TCC GGA GTG TCC CAA GAG ACG ATC GAC	321
Lys Glu Cys Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp	
15 20 25	
AAA GTC CGC ACA GGT GTC TTG GTC GAT GAT CCC AAA ATG AAG AAG	366
Lys Val Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys	
30 35 40	
CAC GTC CTC TGC TTC TCG AAG AAA ACT GGA GTG GCA ACC GAA GCC	411
His Val Leu Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala	
45 50 55	
GGA GAC ACC AAT GTG GAG GTA CTC AAA GCC AAG CTG AAG CAT GTG	456
Gly Asp Thr Asn Val Glu Val Leu Lys Ala Lys Leu Lys His Val	
60 65 70	
GCC AGC GAC GAA GAG GTG GAC AAG ATC GTG CAG AAG TGC GTG GTC	501
Ala Ser Asp Glu Glu Val Asp Lys Ile Val Gln Lys Cys Val Val	
75 80 85	
AAG AAG GCC ACA CCA GAG GAA ACG GCT TAT GAC ACC TTC AAG TGT	546
Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr Asp Thr Phe Lys Cys	
90 95 100	
Stop Codon	
ATT TAC GAC AGT AAA CCT GAT TTC TCT CCT ATT GAT TAA TTGTTTGT	595
Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro Ile Asp *	
105 110 115	
Polyadenylation signal Poly-A tail	
TTTGACTGAA TTTTGACAAT AAAGGTAATA TCGTTATGTA AAAAAAAAAA	645
AAAAAACTCG AGCACCACCA CCACCACCAC TGAGAT	681

Fig. 5.7

His-tagged clone 2.2 without signal sequence															
TTGTTAGCGG	ATGGAATTCC	CTCGTAGGGG	ATAATTTTGT	TTACTTTAAG										50	
His-tag Start Codon															
AAGGAGATAT	ACC	ATG	GGC	AGC	AGC	CAT	CAT	CAT	CAT	CAT	CAC	AGC		96	
	Met	Gly	Ser	Ser	His	His	His	His	His	His	His	Ser			
						-30						-25			
AGC	GGC	CTG	GTG	CCG	CGC	GGC	AGC	CAT	ATG	GCT	AGC	ATG	ACT	GGT	141
Ser	Gly	Leu	Val	Pro	Arg	Gly	Ser	His	Met	Ala	Ser	Met	Thr	Gly	
			-20						-15				-10		
N-terminal of mature AFP															
GGA	CAG	CAA	ATG	GGT	CGC	GGA	TCC	CTC	ACC	GAC	GAA	CAG	ATA	CAG	186
Gly	Gln	Gln	Met	Gly	Arg	Gly	Ser	Leu	Thr	Asp	Glu	Gln	Ile	Gln	
			-5					1				5			
AAA	AGG	AAC	AAG	ATC	AGC	AAA	GAA	TGC	CAG	CAG	GTG	TCC	GGA	GTG	231
Lys	Arg	Asn	Lys	Ile	Ser	Lys	Glu	Cys	Gln	Gln	Val	Ser	Gly	Val	
		10					15					20			
TCC	CAA	GAG	ACG	ATC	GAC	AAA	GTC	CGC	ACA	GGT	GTC	TTG	GTC	GAT	276
Ser	Gln	Glu	Thr	Ile	Asp	Lys	Val	Arg	Thr	Gly	Val	Leu	Val	Asp	
		25					30					35			
GAT	CCC	AAA	ATG	AAG	AAG	CAC	GTC	CTC	TGC	TTC	TCG	AAG	AAA	ACT	321
Asp	Pro	Lys	Met	Lys	Lys	His	Val	Leu	Cys	Phe	Ser	Lys	Lys	Thr	
		40					45					50			
GGA	GTG	GCA	ACC	GAA	GCC	GGA	GAC	ACC	AAT	GTG	GAG	GTA	CTC	AAA	366
Gly	Val	Ala	Thr	Glu	Ala	Gly	Asp	Thr	Asn	Val	Glu	Val	Leu	Lys	
		55					60					65			
GCC	AAG	CTG	AAG	CAT	GTG	GCC	AGC	GAC	GAA	GAG	GTG	GAC	AAG	ATC	411
Ala	Lys	Leu	Lys	His	Val	Ala	Ser	Asp	Glu	Glu	Val	Asp	Lys	Ile	
		70					75					80			
GTG	CAG	AAG	TGC	GTG	GTC	AAG	AAG	GCC	ACA	CCA	GAG	GAA	ACG	GCT	456
Val	Gln	Lys	Cys	Val	Val	Lys	Lys	Ala	Thr	Pro	Glu	Glu	Thr	Ala	
		85					90					95			
TAT	GAC	ACC	TTC	AAG	TGT	ATT	TAC	GAC	AGT	AAA	CCT	GAT	TTC	TCT	501
Tyr	Asp	Thr	Phe	Lys	Cys	Ile	Tyr	Asp	Ser	Lys	Pro	Asp	Phe	Ser	
		100					105					110			
Stop Codon															
CCT	ATT	GAT	TAA	CTCGAGCACC	ACCACCACCA	CCACTGAGAT									543
Pro	Ile	Asp	*												
		115													

Fig. 5.8

His-tagged clone 2.3 with signal sequence

TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTACTTTAAG 50

His-tag Start Codon

AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAC AGC 96
Met Gly Ser Ser His His His His His Ser
-55 -50

AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT 141
Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly
-45 -40 -35

AFP Start Codon

GGA CAG CAA ATG GGT CGC GGA TCC GAA TTC GCA CGA GCA AAA ATG 186
Gly Gln Gln Met Gly Arg Gly Ser Glu Phe Ala Arg Ala Lys Met
-30 -25 -20

AAA CTC CTC TTG TGC TTT GCT TTC GCC GCC ATC GTC ATC GGA GCT 231
Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala Ile Val Ile Gly Ala
-15 -10 -5

N-terminal of Mature AFP

CAG GCT CTC ACC GAC GAA CAG ATA CAG AAA AGG AAC AAG ATC AGC 276
Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser
1 5 10

AAA GAA TGC CAG CAG GTG TCC GGA GTG TCC CAA GAG ACG ATC GAC 321
Lys Glu Cys Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp
15 20 25

AAA GTC CGC ACA GGT GTC TTG GTC GAT GAT CCC AAA ATG AAG AAG 366
Lys Val Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys
30 35 40

CAC GTC CTC TGC TTC TCG AAG AAA ACT GGA GTG GCA ACC GAA GCC 411
His Val Leu Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala
45 50 55

GGA GAC ACC AAT GTG GAG GTA CTC AAA GCC AAG CTG AAG CAT GTG 456
Gly Asp Thr Asn Val Glu Val Leu Lys Ala Lys Leu Lys His Val
60 65 70

GCC AGC GAC GAA GAA GTG GAC AAG ATC GTG CAG AAG TGC GTG GTC 501
Ala Ser Asp Glu Glu Val Asp Lys Ile Val Gln Lys Cys Val Val
75 80 85

AAG AAG GCC ACA CCA GAG GAA ACG GCT TAT GAC ACC TTC AAG TGT 546
Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr Asp Thr Phe Lys Cys
90 95 100

Stop Codon

ATT TAC GAC AGT AAA CCT GAT TTC TCT CCT ATT GAT TAA TTGTTTGTGTA 595
Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro Ile Asp *
105 110 115

Polyadenylation signal Poly-A tail

TTTGACTGAA TTTTGACAAT AAAGGTACTA TCGTTATGAA AAAAAAAAAA 645

AAAAAAAACTC GAGCACCACC ACCACCACCA CTGAGAT 682

Fig. 5.9

His-tagged Clone 2.3 without signal sequence

TTGTTAGCGG ATGGAATTC CTCGTAGGGG ATAATTTTGT TTACTTTAAG	50
His-tag Start Codon	
AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAC AGC	96
Met Gly Ser Ser His His His His His His Ser	
-30 -25	
AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT	141
Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly	
-20 -15 -10	
N-terminal of mature AFP	
GGA CAG CAA ATG GGT CGC GGA TCC CTC ACC GAC GAA CAG ATA CAG	186
Gly Gln Gln Met Gly Arg Gly Ser Leu Thr Asp Glu Gln Ile Gln	
-5 1 5	
AAA AGG AAC AAG ATC AGC AAA GAA TGC CAG CAG GTG TCC GGA GTG	231
Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val	
10 15 20	
TCC CAA GAG ACG ATC GAC AAA GTC CGC ACA GGT GTC TTG GTC GAT	276
Ser Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp	
25 30 35	
GAT CCC AAA ATG AAG AAG CAC GTC CTC TGC TTC TCG AAG AAA ACT	321
Asp Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr	
40 45 50	
GGA GTG GCA ACC GAA GCC GGA GAC ACC AAT GTG GAG GTA CTC AAA	366
Gly Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys	
55 60 65	
GCC AAG CTG AAG CAT GTG GCC AGC GAC GAA GAA GTG GAC AAG ATC	411
Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile	
70 75 80	
GTG CAG AAG TGC GTG GTC AAG AAG GCC ACA CCA GAG GAA ACG GCT	456
Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala	
85 90 95	
TAT GAC ACC TTC AAG TGT ATT TAC GAC AGT AAA CCT GAT TTC TCT	501
Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser	
100 105 110	
Stop Codon	
CCT ATT GAT TAA CTCGAGCACC ACCACCACCA CCACTGAGAT	543
Pro Ile Asp *	
115	

Fig. 5.10

His-tagged Tm 13.17 with signal sequence		
TTGTTAGCGG ATGGAATTC CTCGTAGGGG ATAATTTTGT TTACTTTAAG		50
His-tag Start Codon		
AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAC AGC		96
Met Gly Ser Ser His His His His His Ser		
-65 -60 -55		
AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT		141
Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly		
-50 -45 -40		
GGA CAG CAA ATG GGT CGC GGA TCC GAA TTC TGG ATC CAA AGA ATT		186
Gly Gln Gln Met Gly Arg Gly Ser Glu Phe Trp Ile Gln Arg Ile		
-35 -30 -25		
AFP Start Codon		
CGG CAC GAG ACT ACT AAG ATG AAG TTG CTC TGT TGT CTA ATC TCC		231
Arg His Glu Thr Thr Lys Met Lys Leu Leu Cys Cys Leu Ile Ser		
-20 -15 -10		
N-terminal of mature AFP		
CTC ATT CTG TTG GTC ACA GTT CAG GCC CTG ACC GAG GCA CAA ATT		276
Leu Ile Leu Leu Val Thr Val Gln Ala Leu Thr Glu Ala Gln Ile		
-5 1 5		
GAG AAA CTG AAC AAG ATC AGC AAA AAA TGT CAA AAT GAA AGT GGA		321
Glu Lys Leu Asn Lys Ile Ser Lys Lys Cys Gln Asn Glu Ser Gly		
10 15 20		
GTG TCG CAA GAG ATC ATA ACC AAA GCT CGC AAC GGT GAC TGG GAG		366
Val Ser Gln Glu Ile Ile Thr Lys Ala Arg Asn Gly Asp Trp Glu		
25 30 35		
GAC GAT CCT AAA CTG AAA CGC CAA GTT TTT TGC GTG GCC AGG AAC		411
Asp Asp Pro Lys Leu Lys Arg Gln Val Phe Cys Val Ala Arg Asn		
40 45 50		
GCC GGT CTG GCC ACG GAA TCG GGA GAG GTG GTG GTC GAC GTG TTG		456
Ala Gly Leu Ala Thr Glu Ser Gly Glu Val Val Val Asp Val Leu		
55 60 65		
AGG GAG AAG GTG AGG AAG GTC ACT GAC AAC GAC GAA GAA ACT GAG		501
Arg Glu Lys Val Arg Lys Val Thr Asp Asn Asp Glu Glu Thr Glu		
70 75 80		
AAA ATC ATC AAT AAG TGC GCC GTC AAG AGA GAT ACT GTT GAA GAG		546
Lys Ile Ile Asn Lys Cys Ala Val Lys Arg Asp Thr Val Glu Glu		
85 90 95		
ACG GTG TTC AAT ACT TTC AAA TGT GTC ATG AAA AAC AAG CCA AAG		595
Thr Val Phe Asn Thr Phe Lys Cys Val Met Lys Asn Lys Pro Lys		
100 105 110		
Stop Codon		
TTC TCA CCA GTT GAT TGA ACCACCACGA CTAGTAGATG GTTCAAATGG		643
Phe Ser Pro Val Asp *		
115		
Polyadenylation signal Poly-A tail		
TGTGCTTTAC ATATAAAAT AAAGTGTTC TGATGTAAAA AAAAAAAAAA		693
AAAAAAAAA AACTCGAGAG TATTCTAGAG CGGCCGCGGG CCCATCGTTT		743
TCCACCCCTC GAGCACCACC ACCACCACCA CTGAGAT		777

Fig. 5.11

His-tagged Tm 13.17 without signal sequence

TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTACTTTAAG 50

His-tag Start Codon

AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC 96

Met Gly Ser Ser His His His His His His Ser
-30 -25

AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT 141
Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly
-20 -15 -10

N-terminal of mature AFP

GGA CAG CAA ATG GGT CGC GGC CTG ACC GAG GCA CAA ATT GAG AAA 186
Gly Gln Gln Met Gly Arg Gly Leu Thr Glu Ala Gln Ile Glu Lys
-5 1 5

CTG AAC AAG ATC AGC AAA AAA TGT CAA AAT GAA AGT GGA GTG TCG 231
Leu Asn Lys Ile Ser Lys Lys Cys Gln Asn Glu Ser Gly Val Ser
10 15 20

CAA GAG ATC ATA ACC AAA GCT CGC AAC GGT GAC TGG GAG GAC GAT 276
Gln Glu Ile Ile Thr Lys Ala Arg Asn Gly Asp Trp Glu Asp Asp
25 30 35

CCT AAA CTG AAA CGC CAA GTT TTT TGC GTG GCC AGG AAC GCC GGT 321
Pro Lys Leu Lys Arg Gln Val Phe Cys Val Ala Arg Asn Ala Gly
40 45 50

CTG GCC ACG GAA TCG GGA GAG GTG GTG GTC GAC GTG TTG AGG GAG 366
Leu Ala Thr Glu Ser Gly Glu Val Val Val Asp Val Leu Arg Glu
55 60 65

AAG GTG AGG AAG GTC ACT GAC AAC GAC GAA GAA ACT GAG AAA ATC 411
Lys Val Arg Lys Val Thr Asp Asn Asp Glu Glu Thr Glu Lys Ile
70 75 80

ATC AAT AAG TGC GCC GTC AAG AGA GAT ACT GTT GAA GAG ACG GTG 456
Ile Asn Lys Cys Ala Val Lys Arg Asp Thr Val Glu Glu Thr Val
85 90 95

TTC AAT ACT TTC AAA TGT GTC ATG AAA AAC AAG CCA AAG TTC TCA 501
Phe Asn Thr Phe Lys Cys Val Met Lys Asn Lys Pro Lys Phe Ser
100 105 110

Stop Codon

CCA GTT GAT TGA CTCGAGCACC ACCACCACCA CCACTGAGAT 543
Pro Val Asp *
115

Fig. 5.12

09076348-012802

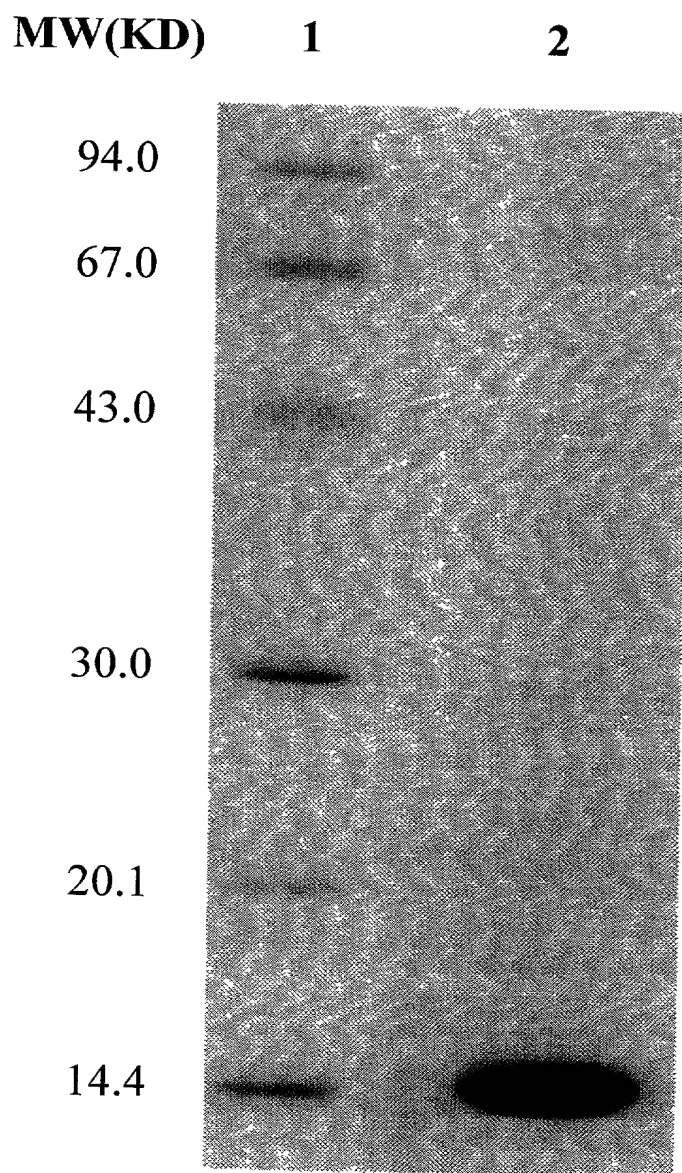


Fig. 6.0

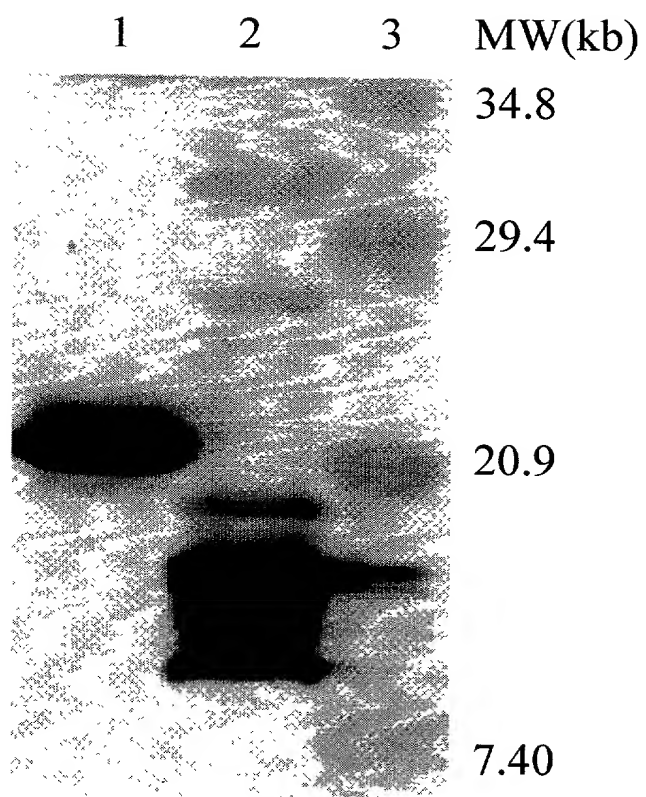


Fig. 6.1

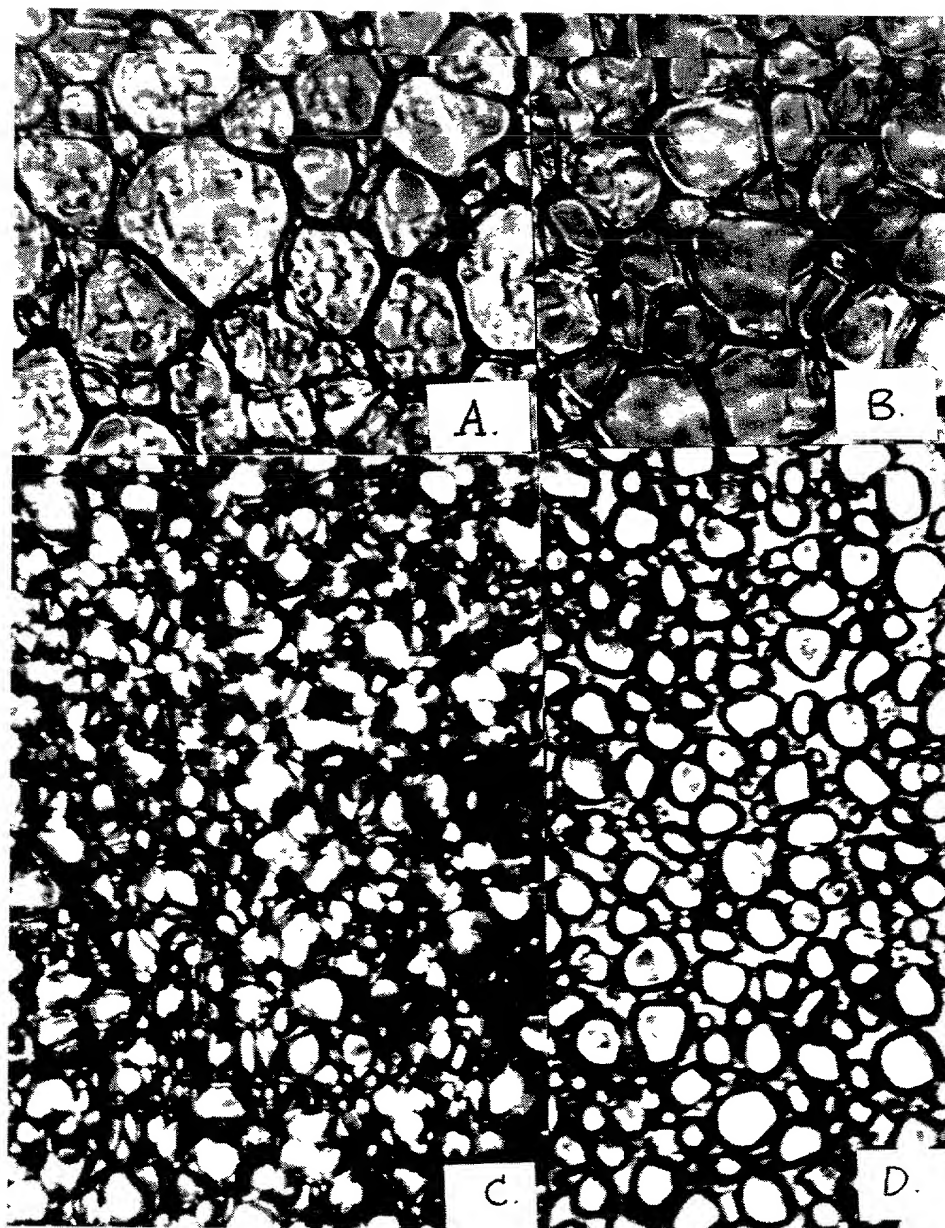


Fig. 6.2

Tm 13.17 S-graph data

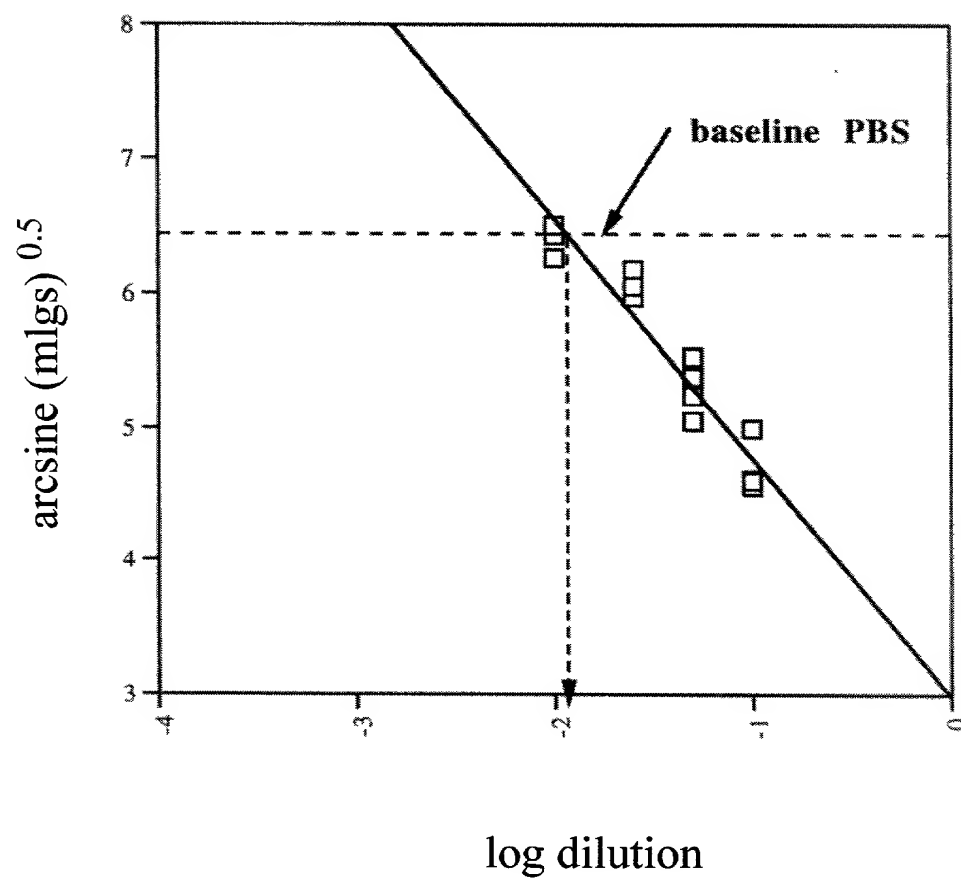


Fig. 6.3

ONE LETTER	NAME	THREE LETTER	CHEMICAL CLASS	HYDROPHOBICITY	Reactivity
A	Alanine	Ala	aliphatic	mod. hydrophobic	low
B	Asp or Asn	Asx			
C	Cysteine	Cys	sulfhydryl	hydrophobic	high
D	Aspartic Acid	Asp	acidic	highly hydrophilic	high
E	Glutamic Acid	Glu	acidic	highly hydrophilic	high
F	Phenylalanine	Phe	aromatic	highly hydrophobic	low
G	Glycine	Gly	aliphatic	mod. hydrophobic	low
H	Histidine	His	basic, imidazole	highly hydrophilic	high
I	Isoleucine	Ile	aliphatic	hydrophobic	low
J					
K	Lysine	Lys	basic	highly hydrophilic	high
L	Leucine	Leu	aliphatic	hydrophobic	low
M	Methionine	Met	sulfhydryl	hydrophobic	low
N	Asparagine	Asn	amide, acidic derived	hydrophilic	high
O					
P	Proline	Pro	aliphatic, cyclic, imino	mod. hydrophilic	low
Q	Glutamine	Gln	amide, acidic derived	hydrophilic	high
R	Arginine	Arg	basic	highly hydrophilic	high
S	Serine	Ser	aliphatic hydroxyl	hydrophilic	high
T	Threonine	Thr	aliphatic hydroxyl	hydrophilic	high
U					
V	Valine	Val	aliphatic	hydrophobic	low
W	Tryptophan	Trp	aromatic	highly hydrophobic	low
X					
Y	Tyrosine	Tyr	aromatic	mod. hydrophilic	high
Z	Glu or Gln	Glx			
		ACD	Any Acidic		
		ALP	Any Aliphatic		
		ALH	Any Aliphatic Hydroxyl		
		ARO	Any Aromatic		
		BAS	Any Basic		
		HY-	Hydrophobic		
		HY+	Hydrophilic		

Fig. 7.1

2022-10-24 10:24:24

Position	Tm12 84-2 2	Tm12 84-2 3	Tm12 84-3 4	Tm12 84-3 9	Tm12 84-7 5	Consensus of Tm12 84	Tm13 17	Consensus with Tm 13 17	B1	Consensus with B1	AFP-3	Consensus with AFP-3
1	A	A	A	A	A	A	A	A		A	C	N
2	C	G	G	G	G	C	G	N		N	G	R
3	G	A	A	A	A	G	A	R		R	A	N
4	A	G	G	G	G	A	C	N		N	G	R
5	A	G	G	G	G	A	T	N		N	A	N
6	C	C	C	C	C	C	A	N		N	C	N
7	A	A	A	A	A	A	C	N		N	C	N
8	A	A	A	A	A	A	T	N		N	G	N
9	A	A	A	A	A	A	A	A		N	A	A
10	A	A	A	A	A	A	A	A		A	A	R
11	A	A	A	A	A	A	*	R		*	G	*
12												
13	A	A	A	A	A	A	A	A	A ² T ² G ²	A	A	A
14	T	T	T	T	T	T	T	T		T	T	T
15	G	G	G	G	G	G	G	G		G	G	G
16	A	A	A	A	A	A	A	A		A	A	A
17	A	A	A	A	A	A	A	A		A	A	A
18	A	A	A	A	A	A	A	A		A	A	A
19	C	C	C	C	C	C	T	T		R	C	R
20	T	T	T	T	T	T	G	C/G		Y	T	T
21	C	C	C	C	C	C	C	C		T	C	C
22	C	C	C	C	C	C	T	C		C	C	C
23	T	T	T	T	T	T	T	T		T	T	T
24	T	T	T	T	T	T	T	T		T	T	T
25	T	T	T	T	T	T	T	T		T	T	T
26	T	T	T	T	T	T	T	T		T	T	T
27	G	G	G	G	G	G	T	T		N	C	N
28	T	T	T	T	T	T	G	T		N	T	N
29	G	G	G	G	G	G	T	T		T	G	T
30	C	C	C	C	C	C	T	T		Y	T	Y
31	T	T	T	T	T	T	T	T		T	T	T
32	T	T	T	T	T	T	A	T		T	T	T
33	T	T	T	T	T	T	A	T	T/A	T/A	T	T/A
34	G	G	G	G	G	G	T	T	R	R	T	R
35	C	C	C	C	C	C	T	T	N	N	C	N
36	T	T	T	T	T	T	T	T	Y	Y	C	Y
37	T	T	T	T	T	T	C	C	C	C	T	C
38	T	T	T	T	T	T	C	C	C	C	T	C
39	T	T	T	T	T	T	C	C	C	C	T	C
40	G	G	G	G	G	G	C	C	G/C	G/C	G	G/C
41	C	C	C	C	C	C	C	C	Y	Y	T	Y
42	C	C	C	C	C	C	C	C	C	C	T	C
43	C	C	C	C	C	C	C	C	R	R	C	R
44	C	C	C	C	C	C	C	C	Y	Y	C	Y
45	C	C	C	C	C	C	C	C	Y	Y	C	Y
46	A	A	A	A	A	A	T	T	N	N	T	N
47	T	T	T	T	T	T	T	T	C/G	C/G	T	C/G
48	C	C	C	C	C	C	G	G	N	N	G	N
49	G	G	G	G	G	G	T	T	T	T	C	T
50	T	T	T	T	T	T	G	G	C/G	C/G	T	C/G
51	C	C	C	C	C	C	G	G	R	R	C	R
52	A	A	A	A	A	A	T	T	C	C	G	C
53	T	T	T	T	T	T	C	C	R	R	C	R
54	C	C	C	C	C	C	A	A	G/C	G/C	C	C
55	G	G	G	G	G	G	C	C	A	A	C	A
56	A	A	A	A	A	A	G	G	Y	Y	C	Y
57	G	G	G	G	G	G	T	T	A	A	C	A
58	C	C	C	C	C	C	C	C	G	G	A	G
59	T	T	T	T	T	T	C	C	T	T	C	T
60	C	C	C	C	C	C	A	A	C	C	A	C
61	A	A	A	A	A	A	G	G	A	A	G	A
62	G	G	G	G	G	G	C	C	A	A	C	A
63	A	A	A	A	A	A	G	G	C	C	T	C
64	G	G	G	G	G	G	C	C	Y	Y	N	Y
65	C	C	C	C	C	C	T	T	C/G	C/G	T	T
66	T	T	T	T	T	T	C	C	A	A	C	A
67	C	C	C	C	C	C	A	A	C	C	T	C
68	T	T	T	T	T	T	G	G			A	A
69	C	C	C	C	C	C	A	A	C	C	T	T
70	A	A	A	A	A	A	C	C	G	G	A	A
71	C	C	C	C	C	C	G	G	A	A	C	A
72	C	C	C	C	C	C	A	A	G	G	A	A
73	G	G	G	G	G	G	A	A	C	C	A	A
74	A	A	A	A	A	A	C	C	A	A	C	A
75	C	C	C	C	C	C	A	A	G	G	A	A
76	G	G	G	G	G	G	A	A	C	C	A	A
77	A	A	A	A	A	A	A	A	C	C	A	A
78	A	A	A	A	A	A	A	A	C	C	A	A
79	A	A	A	A	A	A	A	A	C	C	A	A
80	A	A	A	A	A	A	A	A	C	C	A	A
81	G	G	G	G	G	G	A	A	R	R	C	C
82	A	A	A	A	A	A	T	T	T	T	G	G
83	T	T	T	T	T	T	A	A	A/G	A/G	A	A
84	C	C	C	C	C	C	G	G	C/G	C/G	T	T
85	A	A	A	A	A	A	A	A	A	A	A	A
86	A	A	A	A	A	A	A	A	A	A	A	A
87	G	G	G	G	G	G	A	A	A	A	A	A
88	A	A	A	A	A	A	A	A	A	A	A	A
89	A	A	A	A	A	A	A	A	A	A	A	A
90	A	A	A	A	A	A	A	A	A	A	A	A
91	A	A	A	A	A	A	A	A	A	A	A	A
92	G	G	G	G	G	G	A	A	N	N	C	N
93	G	G	G	G	G	G	A	A	G	G	A	G
94	A	A	A	A	A	A	C	C	A	A	C	A
95	C	C	C	C	C	C	A	A	C	C	A	A
96	A	A	A	A	A	A	A	A	A	A	A	A
97	A	A	A	A	A	A	A	A	A	A	A	A
98	A	A	A	A	A	A	A	A	A	A	A	A
99	A	A	A	A	A	A	A	A	A	A	A	A
100	A	A	A	A	A	A	A	A	A	A	A	A
101	T	T	T	T	T	T	T	T	A	A	C	A
102	C	C	C	C	C	C	A	A	C	C	A	A
103	A	A	A	A	A	A	G	G	A	A	A	A
104	G	G	G	G	G	G	C	C	A	A	A	A
105	C	C	C	C	C	C	A	A	C	C	A	A
106	A	A	A	A	A	A	A	A	A	A	A	A
107	A	A	A	A	A	A	A	A	A	A	A	A
108	A	A	A	A	A	A	A	A	A	A	A	A
109	G	G	G	G	G	G	A	A	R	R	C	C
110	A	A	A	A	A	A	A	A	A	A	A	A
111	A	A	A	A	A	A	A	A	R	R	T	T
112	T	T	T	T	T	T	T	T	G	G	T	T
113	C	C	C	C	C	C	C	C	Y	Y	C	C
114	C	C	C	C	C	C	C	C	A	A	A	A
115	C	C	C	C	C	C	C	C	A	A	A	A
116	A	A	A	A	A	A	A	A	A	A	A	A
117	G	G	G	G	G	G	A	A	R	R	G	G

Fig. 7.2

Position	Tm12 84-2 2	Tm12 84-2 3	Tm12 84-3 4	Tm12 84-3 9	Tm12 84-7 5	Consensus of	Tm13 17	Consensus with	B1	Consensus with	AFP-3	Consensus with
118	C	C	C	C	C	C	A	N	A	N	G	N
119	A	A	A	A	A	A	T	C	C	N	C	N
120	G	G	G	G	G	G	G	A	T	N	T	N
121	G	G	G	G	G	T/A	A	A	A	G	A	G
122	T	T	T	T	T	C	A	R	A	T/A	R	A/T
123	G	G	G	G	G	C	A	T/A	A	C/G	T	T/A
124	T	T	T	T	T	C	G	C/G	G	C/G	C	C/G
125	C	C	C	C	C	C	T	Y	T	Y	T	Y
126	C	C	C	C	C	G	G	G	G	G	G	G
127	G	G	G	G	G	G	A	A	A	A	A	A
128	A	A	A	A	A	G	G	G	G	G	G	G
129	A	A	A	A	A	T	T	A	T	A	T	A
130	G	G	G	G	G	G	G	G	G	G	G	G
131	T	T	T	T	T	T	T	T	T	T	T	T
132	T	T	T	T	T	C	C	C	C	C	C	C
133	C	C	C	C	C	C	G	C/G	C	C/G	C	C
134	C	C	C	C	C	C	C	C	C	C	C	C
135	C	C	C	C	C	A	A	A	A	A	A	A
136	A	A	A	A	A	A	A	A	A	A	A	A
137	A	A	A	A	A	G	G	G	G	G	G	G
138	A	A	A	A	A	A	A	A	A	A	A	A
139	A	A	A	A	A	A	A	A	A	A	A	A
140	A	A	A	A	A	A	A	A	A	A	A	A
141	A	A	A	A	A	A	A	A	A	A	A	A
142	A	A	A	A	A	A	A	A	A	A	A	A
143	A	A	A	A	A	A	A	A	A	A	A	A
144	A	A	A	A	A	A	A	A	A	A	A	A
145	A	A	A	A	A	A	A	A	A	A	A	A
146	A	A	A	A	A	A	A	A	A	A	A	A
147	A	A	A	A	A	A	A	A	A	A	A	A
148	A	A	A	A	A	A	A	A	A	A	A	A
149	A	A	A	A	A	A	A	A	A	A	A	A
150	A	A	A	A	A	A	A	A	A	A	A	A
151	A	A	A	A	A	A	A	A	A	A	A	A
152	A	A	A	A	A	A	A	A	A	A	A	A
153	A	A	A	A	A	A	A	A	A	A	A	A
154	A	A	A	A	A	A	A	A	A	A	A	A
155	A	A	A	A	A	A	A	A	A	A	A	A
156	A	A	A	A	A	A	A	A	A	A	A	A
157	A	A	A	A	A	A	A	A	A	A	A	A
158	A	A	A	A	A	A	A	A	A	A	A	A
159	A	A	A	A	A	A	A	A	A	A	A	A
160	A	A	A	A	A	A	A	A	A	A	A	A
161	A	A	A	A	A	A	A	A	A	A	A	A
162	A	A	A	A	A	A	A	A	A	A	A	A
163	A	A	A	A	A	A	A	A	A	A	A	A
164	A	A	A	A	A	A	A	A	A	A	A	A
165	A	A	A	A	A	A	A	A	A	A	A	A
166	A	A	A	A	A	A	A	A	A	A	A	A
167	A	A	A	A	A	A	A	A	A	A	A	A
168	A	A	A	A	A	A	A	A	A	A	A	A
169	A	A	A	A	A	A	A	A	A	A	A	A
170	A	A	A	A	A	A	A	A	A	A	A	A
171	A	A	A	A	A	A	A	A	A	A	A	A
172	A	A	A	A	A	A	A	A	A	A	A	A
173	A	A	A	A	A	A	A	A	A	A	A	A
174	A	A	A	A	A	A	A	A	A	A	A	A
175	A	A	A	A	A	A	A	A	A	A	A	A
176	A	A	A	A	A	A	A	A	A	A	A	A
177	A	A	A	A	A	A	A	A	A	A	A	A
178	A	A	A	A	A	A	A	A	A	A	A	A
179	A	A	A	A	A	A	A	A	A	A	A	A
180	A	A	A	A	A	A	A	A	A	A	A	A
181	A	A	A	A	A	A	A	A	A	A	A	A
182	A	A	A	A	A	A	A	A	A	A	A	A
183	A	A	A	A	A	A	A	A	A	A	A	A
184	A	A	A	A	A	A	A	A	A	A	A	A
185	A	A	A	A	A	A	A	A	A	A	A	A
186	A	A	A	A	A	A	A	A	A	A	A	A
187	A	A	A	A	A	A	A	A	A	A	A	A
188	A	A	A	A	A	A	A	A	A	A	A	A
189	A	A	A	A	A	A	A	A	A	A	A	A
190	A	A	A	A	A	A	A	A	A	A	A	A
191	A	A	A	A	A	A	A	A	A	A	A	A
192	A	A	A	A	A	A	A	A	A	A	A	A
193	A	A	A	A	A	A	A	A	A	A	A	A
194	A	A	A	A	A	A	A	A	A	A	A	A
195	A	A	A	A	A	A	A	A	A	A	A	A
196	A	A	A	A	A	A	A	A	A	A	A	A
197	A	A	A	A	A	A	A	A	A	A	A	A
198	A	A	A	A	A	A	A	A	A	A	A	A
199	A	A	A	A	A	A	A	A	A	A	A	A
200	A	A	A	A	A	A	A	A	A	A	A	A
201	A	A	A	A	A	A	A	A	A	A	A	A
202	A	A	A	A	A	A	A	A	A	A	A	A
203	A	A	A	A	A	A	A	A	A	A	A	A
204	A	A	A	A	A	A	A	A	A	A	A	A
205	A	A	A	A	A	A	A	A	A	A	A	A
206	A	A	A	A	A	A	A	A	A	A	A	A
207	A	A	A	A	A	A	A	A	A	A	A	A
208	A	A	A	A	A	A	A	A	A	A	A	A
209	A	A	A	A	A	A	A	A	A	A	A	A
210	A	A	A	A	A	A	A	A	A	A	A	A
211	A	A	A	A	A	A	A	A	A	A	A	A
212	A	A	A	A	A	A	A	A	A	A	A	A
213	A	A	A	A	A	A	A	A	A	A	A	A
214	A	A	A	A	A	A	A	A	A	A	A	A
215	A	A	A	A	A	A	A	A	A	A	A	A
216	A	A	A	A	A	A	A	A	A	A	A	A
217	A	A	A	A	A	A	A	A	A	A	A	A
218	A	A	A	A	A	A	A	A	A	A	A	A
219	A	A	A	A	A	A	A	A	A	A	A	A
220	A	A	A	A	A	A	A	A	A	A	A	A
221	A	A	A	A	A	A	A	A	A	A	A	A
222	A	A	A	A	A	A	A	A	A	A	A	A
223	A	A	A	A	A	A	A	A	A	A	A	A
224	A	A	A	A	A	A	A	A	A	A	A	A
225	A	A	A	A	A	A	A	A	A	A	A	A
226	A	A	A	A	A	A	A	A	A	A	A	A
227	A	A	A	A	A	A	A	A	A	A	A	A
228	A	A	A	A	A	A	A	A	A	A	A	A
229	A	A	A	A	A	A	A	A	A	A	A	A
230	A	A	A	A	A	A	A	A	A	A	A	A
231	A	A	A	A	A	A	A	A	A	A	A	A
232	A	A	A	A	A	A	A	A	A	A	A	A
233	A	A	A	A	A	A	A	A	A	A	A	A
234	A	A	A	A	A	A	A	A	A	A	A	A
235	A	A	A	A	A	A	A	A	A	A	A	A

Fig. 7.2 cont.

Position	Tm12 84-2-2	Tm12 84-2-3	Tm12 84-3-4	Tm12 84-3-9	Tm12 84-7-5	Consensus of	Tm13 17	Consensus with	B1	Consensus with	APF-3	Consensus with
236	A	A	A	A	A	A	A	A	A	A	C	N
237	A	A	A	A	A	A	A	A	A	A	C	N
238	G	G	G	G	G	G	T	N	T	N	C	C
239	C	C	C	C	C	C	C	C	C	C	G	N
240	C	C	C	C	C	C	G	G	G	G	G	G
241	G	G	G	G	G	G	G	G	G	G	G	G
242	G	G	G	G	G	G	A	A	A	A	G	A
243	A	A	A	A	A	A	G	G	G	G	A	A
244	A	A	A	A	A	A	G	A	A	A	A	A
245	A	A	A	A	A	A	G	A	A	A	A	A
246	C	C	C	C	C	C	G	C	A	N	A	N
247	A	A	A	A	A	A	T	R	A	R	A	N
248	C	C	C	C	C	C	T	Y	T	Y	C	N
249	A	A	A	A	A	A	G	C	T	N	C	N
250	A	A	A	A	A	A	T	R	A	A	A	A
251	A	A	A	A	A	A	T	A	A	A	A	A
252	T	T	T	T	T	T	G	N	G	A	A	A
253	T	T	T	T	T	T	G	T	C	N	C	G
254	G	G	G	G	G	G	A	G	G	G	O	G
255	G	G	G	G	G	G	A	G	A	G	A	G
256	G	G	G	G	G	G	A	G	A	G	A	G
257	A	A	A	A	A	A	G	G	C	C	C	C
258	G	G	G	G	G	G	T	R	C	G	A	A
259	T	T	T	T	T	T	T	Y	T	R	A	A
260	A	A	A	A	A	A	T	T	T	T	T	T
261	C	C	C	C	C	C	T	T	T	T	T	T
262	T	T	T	T	T	T	C	A	A	A	T	T
263	C	C	C	C	C	C	A	A	A	A	A	A
264	A	A	A	A	A	A	A	A	A	A	A	A
265	A	A	A	A	A	A	A	A	A	A	A	A
266	A	A	A	A	A	A	A	A	A	A	A	A
267	A	A	A	A	A	A	A	A	A	A	A	A
268	G	G	G	G	G	G	A	G	A	G	A	A
269	C	C	C	C	C	C	A	C	A	C	A	A
270	C	C	C	C	C	C	A	C	A	C	A	A
271	A	A	A	A	A	A	A	A	A	A	A	A
272	A	A	A	A	A	A	A	A	A	A	A	A
273	G	G	G	G	G	G	T	G	T	G	T	G
274	T	T	T	T	T	T	A	A	A	A	A	A
275	G	G	G	G	G	G	A	A	A	A	A	A
276	A	A	A	A	A	A	A	A	A	A	A	A
277	A	A	A	A	A	A	A	A	A	A	A	A
278	A	A	A	A	A	A	A	A	A	A	A	A
279	A	A	A	A	A	A	A	A	A	A	A	A
280	C	C	C	C	C	C	A	A	A	A	A	A
281	A	A	A	A	A	A	T	T	T	T	T	T
282	T	T	T	T	T	T	G	G	G	G	G	G
283	T	T	T	T	T	T	G	G	G	G	G	G
284	G	G	G	G	G	G	T	T	T	T	T	T
285	G	G	G	G	G	G	T	T	T	T	T	T
286	G	G	G	G	G	G	T	T	T	T	T	T
287	C	C	C	C	C	C	C	C	C	C	C	C
288	C	C	C	C	C	C	C	C	C	C	C	C
289	A	A	A	A	A	A	A	A	A	A	A	A
290	G	G	G	G	G	G	A	A	A	A	A	A
291	C	C	C	C	C	C	A	A	A	A	A	A
292							A	A	A	A	A	A
293							A	A	A	A	A	A
294							A	A	A	A	A	A
295	G	G	G	G	G	G	A	A	A	A	A	A
296	A	A	A	A	A	A	A	A	A	A	A	A
297	A	A	A	A	A	A	A	A	A	A	A	A
298	A	A	A	A	A	A	A	A	A	A	A	A
299	A	A	A	A	A	A	A	A	A	A	A	A
300	A	A	A	A	A	A	A	A	A	A	A	A
301	A	A	A	A	A	A	A	A	A	A	A	A
302	A	A	A	A	A	A	A	A	A	A	A	A
303	A	A	A	A	A	A	A	A	A	A	A	A
304	A	A	A	A	A	A	A	A	A	A	A	A
305	T	T	T	T	T	T	A	A	A	A	A	A
306	G	G	G	G	G	G	A	A	A	A	A	A
307	A	A	A	A	A	A	A	A	A	A	A	A
308	A	A	A	A	A	A	A	A	A	A	A	A
309	A	A	A	A	A	A	A	A	A	A	A	A
310	A	A	A	A	A	A	A	A	A	A	A	A
311	A	A	A	A	A	A	A	A	A	A	A	A
312	A	A	A	A	A	A	A	A	A	A	A	A
313	T	T	T	T	T	T	C	C	C	C	C	C
314	T	T	T	T	T	T	C	C	C	C	C	C
315	C	C	C	C	C	C	T	T	T	T	T	T
316	T	T	T	T	T	T	C	C	C	C	C	C
317	T	T	T	T	T	T	C	C	C	C	C	C
318	G	G	G	G	G	G	A	A	A	A	A	A
319	A	A	A	A	A	A	A	A	A	A	A	A
320	A	A	A	A	A	A	A	A	A	A	A	A
321	A	A	A	A	A	A	A	A	A	A	A	A
322	A	A	A	A	A	A	A	A	A	A	A	A
323	A	A	A	A	A	A	A	A	A	A	A	A
324	T	T	T	T	T	T	G	G	G	G	G	G
325	G	G	G	G	G	G	C	C	C	C	C	C
326	C	C	C	C	C	C	G	G	G	G	G	G
327	G	G	G	G	G	G	T	T	T	T	T	T
328	T	T	T	T	T	T	G	G	G	G	G	G
329	T	T	T	T	T	T	G	G	G	G	G	G
330	G	G	G	G	G	G	T	T	T	T	T	T
331	G	G	G	G	G	G	T	T	T	T	T	T
332	T	T	T	T	T	T	C	C	C	C	C	C
333	C	C	C	C	C	C	A	A	A	A	A	A
334	A	A	A	A	A	A	A	A	A	A	A	A
335	A	A	A	A	A	A	A	A	A	A	A	A
336	A	A	A	A	A	A	A	A	A	A	A	A
337	A	A	A	A	A	A	A	A	A	A	A	A
338	A	A	A	A	A	A	A	A	A	A	A	A
339	G	G	G	G	G	G	A	A	A	A	A	A
340	G	G	G	G	G	G	A	A	A	A	A	A
341	C	C	C	C	C	C	A	A	A	A	A	A
342	C	C	C	C	C	C	A	A	A	A	A	A
343	A	A	A	A	A	A	A	A	A	A	A	A
344	C	C	C	C	C	C	A	A	A	A	A	A
345	C	C	C	C	C	C	A	A	A	A	A	A
346	C	C	C	C	C	C	A	A	A	A	A	A
347	A	A	A	A	A	A	A	A	A	A	A	A
348	A	A	A	A	A	A	A	A	A	A	A	A
349	A	A	A	A	A	A	A	A	A	A	A	A
350	A	A	A	A	A	A	A	A	A	A	A	A
351	A	A	A	A	A	A	A	A	A	A	A	A
352	A	A	A	A	A	A	A	A	A	A	A	A
353	A	A	A	A	A	A	A	A	A	A	A	A

Fig. 7.2 cont.

Position	Tm12 84-2 2	Tm12 84-2 3	Tm12 84-3 4	Tm12 84-3 9	Tm12 84-7 5	Consensus of	Tm13 17	Consensus with	B1	Consensus with	AFP-3	Consensus with
354	A	A	A	A	A	A	G	A	A	N	C	N
355	A	A	A	A	A	A	A	A	C	N	T	N
356	C	C	C	C	C	C	C	C	G	C/G	C	C/G
357	G	G	G	G	G	G	G	G	C	G/C	T	N
358	C	C	C	C	C	C	C	C	A	N	C	N
359	T	T	T	T	T	T	T	T	T	N	A	N
360	T	T	T	T	T	T	T	T	T	N	C	N
361	T	T	T	T	T	T	T	T	T	N	G	N
362	T	T	T	T	T	T	T	T	T	N	C	N
363	T	T	T	T	T	T	T	T	T	N	C	N
364	G	G	G	G	G	G	A	A	A	A/T	G	N
365	A	A	A	A	A	A	A	A	A	N	G	N
366	C	C	C	C	C	C	A	A	A	N	A	N
367	A	A	A	A	A	A	T	T	T	A/T	C	A/T
368	C	C	C	C	C	C	A	A	T	N	T	N
369	C	C	C	C	C	C	C	C	T	N	T	N
370	T	T	T	T	T	T	T	T	A	N	T	N
371	T	T	T	T	T	T	T	T	C	N	T	N
372	C	C	C	C	C	C	A	A	A	N	T	N
373	A	A	A	A	A	A	A	A	A	N	A	N
374	G	G	G	G	G	G	A	A	A	N	A	N
375	T	T	T	T	T	T	A	A	T	N	T	N
376	T	T	T	T	T	T	G	G	T	N	G	N
377	G	G	G	G	G	G	T	T	T	N	C	N
378	T	T	T	T	T	T	G	G	T	N	T	N
379	T	T	T	T	T	T	T	T	T	N	T	N
380	T	T	T	T	T	T	T	T	T	N	T	N
381	T	T	T	T	T	T	T	T	T	N	T	N
382	T	T	T	T	T	T	T	T	T	N	T	N
383	A	A	A	A	A	A	A	A	A	N	C	N
384	C	C	C	C	C	C	G	G	A	N	A	N
385	G	G	G	G	G	G	A	A	G	N	C	N
386	C	C	C	C	C	C	A	A	G	N	A	N
387	A	A	A	A	A	A	A	A	A	N	A	N
388	C	C	C	C	C	C	A	A	A	N	A	N
389	G	G	G	G	G	G	A	A	A	N	A	N
390	C	C	C	C	C	C	A	A	A	N	A	N
391	A	A	A	A	A	A	A	A	A	N	A	N
392	A	A	A	A	A	A	A	A	A	N	A	N
393	A	A	A	A	A	A	A	A	A	N	A	N
394	C	C	C	C	C	C	C	C	C	N	G	N
395	C	C	C	C	C	C	C	C	C	N	T	N
396	T	T	T	T	T	T	A	A	A	N	C	N
397	G	G	G	G	G	G	A	A	A	N	G	N
398	A	A	A	A	A	A	A	A	A	N	T	N
399	T	T	T	T	T	T	T	T	T	N	T	N
400	T	T	T	T	T	T	T	T	T	N	T	N
401	T	T	T	T	T	T	T	T	T	N	T	N
402	T	T	T	T	T	T	T	T	T	N	T	N
403	T	T	T	T	T	T	T	T	T	N	T	N
404	T	T	T	T	T	T	T	T	T	N	T	N
405	T	T	T	T	T	T	T	T	T	N	T	N
406	T	T	T	T	T	T	T	T	T	N	T	N
407	T	T	T	T	T	T	T	T	T	N	T	N
408	T	T	T	T	T	T	T	T	T	N	T	N
409	T	T	T	T	T	T	T	T	T	N	T	N
410	T	T	T	T	T	T	T	T	T	N	T	N
411	T	T	T	T	T	T	T	T	T	N	T	N
412	T	T	T	T	T	T	T	T	T	N	T	N
413	T	T	T	T	T	T	T	T	T	N	T	N
414	T	T	T	T	T	T	T	T	T	N	T	N
415	T	T	T	T	T	T	T	T	T	N	T	N
416	T	T	T	T	T	T	T	T	T	N	T	N
417	T	T	T	T	T	T	T	T	T	N	T	N
418	T	T	T	T	T	T	T	T	T	N	T	N
419	T	T	T	T	T	T	T	T	T	N	T	N
420	T	T	T	T	T	T	T	T	T	N	T	N
421	T	T	T	T	T	T	T	T	T	N	T	N
422	T	T	T	T	T	T	T	T	T	N	T	N
423	T	T	T	T	T	T	T	T	T	N	T	N
424	T	T	T	T	T	T	T	T	T	N	T	N
425	T	T	T	T	T	T	T	T	T	N	T	N
426	T	T	T	T	T	T	T	T	T	N	T	N
427	T	T	T	T	T	T	T	T	T	N	T	N
428	T	T	T	T	T	T	T	T	T	N	T	N
429	T	T	T	T	T	T	T	T	T	N	T	N
430	T	T	T	T	T	T	T	T	T	N	T	N
431	T	T	T	T	T	T	T	T	T	N	T	N
432	T	T	T	T	T	T	T	T	T	N	T	N
433	T	T	T	T	T	T	T	T	T	N	T	N
434	T	T	T	T	T	T	T	T	T	N	T	N
435	T	T	T	T	T	T	T	T	T	N	T	N
436	T	T	T	T	T	T	T	T	T	N	T	N
437	T	T	T	T	T	T	T	T	T	N	T	N
438	T	T	T	T	T	T	T	T	T	N	T	N
439	T	T	T	T	T	T	T	T	T	N	T	N
440	T	T	T	T	T	T	T	T	T	N	T	N
441	T	T	T	T	T	T	T	T	T	N	T	N
442	T	T	T	T	T	T	T	T	T	N	T	N
443	T	T	T	T	T	T	T	T	T	N	T	N
444	T	T	T	T	T	T	T	T	T	N	T	N
445	T	T	T	T	T	T	T	T	T	N	T	N
446	T	T	T	T	T	T	T	T	T	N	T	N
447	T	T	T	T	T	T	T	T	T	N	T	N
448	T	T	T	T	T	T	T	T	T	N	T	N
449	T	T	T	T	T	T	T	T	T	N	T	N
450	T	T	T	T	T	T	T	T	T	N	T	N
451	T	T	T	T	T	T	T	T	T	N	T	N
452	T	T	T	T	T	T	T	T	T	N	T	N
453	T	T	T	T	T	T	T	T	T	N	T	N
454	T	T	T	T	T	T	T	T	T	N	T	N
455	T	T	T	T	T	T	T	T	T	N	T	N
456	T	T	T	T	T	T	T	T	T	N	T	N
457	T	T	T	T	T	T	T	T	T	N	T	N
458	T	T	T	T	T	T	T	T	T	N	T	N
459	T	T	T	T	T	T	T	T	T	N	T	N
460	T	T	T	T	T	T	T	T	T	N	T	N
461	T	T	T	T	T	T	T	T	T	N	T	N
462	T	T	T	T	T	T	T	T	T	N	T	N
463	T	T	T	T	T	T	T	T	T	N	T	N
464	T	T	T	T	T	T	T	T	T	N	T	N
465	T	T	T	T	T	T	T	T	T	N	T	N
466	T	T	T	T	T	T	T	T	T	N	T	N
467	T	T	T	T	T	T	T	T	T	N	T	N
468	T	T	T	T	T	T	T	T	T	N	T	N
469	T	T	T	T	T	T	T	T	T	N	T	N
470	T	T	T	T	T	T	T	T	T	N	T	N
471	T	T	T	T	T	T	T	T	T	N	T	N

Fig. 7.2 cont.

Position	Tm 12.84-2.2	Tm 12.84-2.3	Tm 12.84-3.4	Tm 12.84-3.9	Tm 12.84-7.5	Tm 13.17	Consensus Tm 13.17	Tm P-91	Tm P-92	Consensus Tm P-92	Tm AFP-3	Consensus Tm AFP-3	GENERAL CONSENSUS	SUBSTITUTIONS - most to least common
1	M	M	M	M	M	M	M	L	L	HY, ALPHALP	M	M	K	C
2	K	K	K	K	K	K	K	L	L	K	K	K	K	L
3	L	L	L	L	L	L	L	L	L	K	L	L	L	L
4	L	L	L	L	L	L	L	L	L	K	L	L	L	L
5	L	L	L	L	L	L	L	L	L	K	L	L	L	L
6	L	L	L	L	L	L	L	L	L	K	L	L	L	L
7	L	L	L	L	L	L	L	L	L	K	L	L	L	L
8	L	L	L	L	L	L	L	L	L	K	L	L	L	L
9	L	L	L	L	L	L	L	L	L	K	L	L	L	L
10	L	L	L	L	L	L	L	L	L	K	L	L	L	L
11	L	L	L	L	L	L	L	L	L	K	L	L	L	L
12	L	L	L	L	L	L	L	L	L	K	L	L	L	L
13	L	L	L	L	L	L	L	L	L	K	L	L	L	L
14	L	L	L	L	L	L	L	L	L	K	L	L	L	L
15	L	L	L	L	L	L	L	L	L	K	L	L	L	L
16	L	L	L	L	L	L	L	L	L	K	L	L	L	L
17	L	L	L	L	L	L	L	L	L	K	L	L	L	L
18	L	L	L	L	L	L	L	L	L	K	L	L	L	L
19	L	L	L	L	L	L	L	L	L	K	L	L	L	L
20	L	L	L	L	L	L	L	L	L	K	L	L	L	L
21	L	L	L	L	L	L	L	L	L	K	L	L	L	L
22	L	L	L	L	L	L	L	L	L	K	L	L	L	L
23	L	L	L	L	L	L	L	L	L	K	L	L	L	L
24	L	L	L	L	L	L	L	L	L	K	L	L	L	L
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26	L	L	L	L	L	L	L	L	L	K	L	L	L	L
27	L	L	L	L	L	L	L	L	L	K	L	L	L	L
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29	L	L	L	L	L	L	L	L	L	K	L	L	L	L
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31	L	L	L	L	L	L	L	L	L	K	L	L	L	L
32	L	L	L	L	L	L	L	L	L	K	L	L	L	L
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34	L	L	L	L	L	L	L	L	L	K	L	L	L	L
35	L	L	L	L	L	L	L	L	L	K	L	L	L	L
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37	L	L	L	L	L	L	L	L	L	K	L	L	L	L
38	L	L	L	L	L	L	L	L	L	K	L	L	L	L
39	L	L	L	L	L	L	L	L	L	K	L	L	L	L
40	L	L	L	L	L	L	L	L	L	K	L	L	L	L
41	L	L	L	L	L	L	L	L	L	K	L	L	L	L
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44	L	L	L	L	L	L	L	L	L	K	L	L	L	L
45	L	L	L	L	L	L	L	L	L	K	L	L	L	L
46	L	L	L	L	L	L	L	L	L	K	L	L	L	L
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50	L	L	L	L	L	L	L	L	L	K	L	L	L	L
51	L	L	L	L	L	L	L	L	L	K	L	L	L	L
52	L	L	L	L	L	L	L	L	L	K	L	L	L	L
53	L	L	L	L	L	L	L	L	L	K	L	L	L	L
54	L	L	L	L	L	L	L	L	L	K	L	L	L	L
55	L	L	L	L	L	L	L	L	L	K	L	L	L	L
56	L	L	L	L	L	L	L	L	L	K	L	L	L	L
57	L	L	L	L	L	L	L	L	L	K	L	L	L	L
58	L	L	L	L	L	L	L	L	L	K	L	L	L	L
59	L	L	L	L	L	L	L	L	L	K	L	L	L	L
60	L	L	L	L	L	L	L	L	L	K	L	L	L	L
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62	L	L	L	L	L	L	L	L	L	K	L	L	L	L
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68	L	L	L	L	L	L	L	L	L	K	L	L	L	L
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70	L	L	L	L	L	L	L	L	L	K	L	L	L	L
71	L	L	L	L	L	L	L	L	L	K	L	L	L	L
72	L	L	L	L	L	L	L	L	L	K	L	L	L	L
73	L	L	L	L	L	L	L	L	L	K	L	L	L	L
74	L	L	L	L	L	L	L	L	L	K	L	L	L	L
75	L	L	L	L	L	L	L	L	L	K	L	L	L	L
76	L	L	L	L	L	L	L	L	L	K	L	L	L	L
77	L	L	L	L	L	L	L	L	L	K	L	L	L	L
78	L	L	L	L	L	L	L	L	L	K	L	L	L	L

Fig. 7.3

(3.4) is the only variant in the family)

Fig. 7.3 cont.

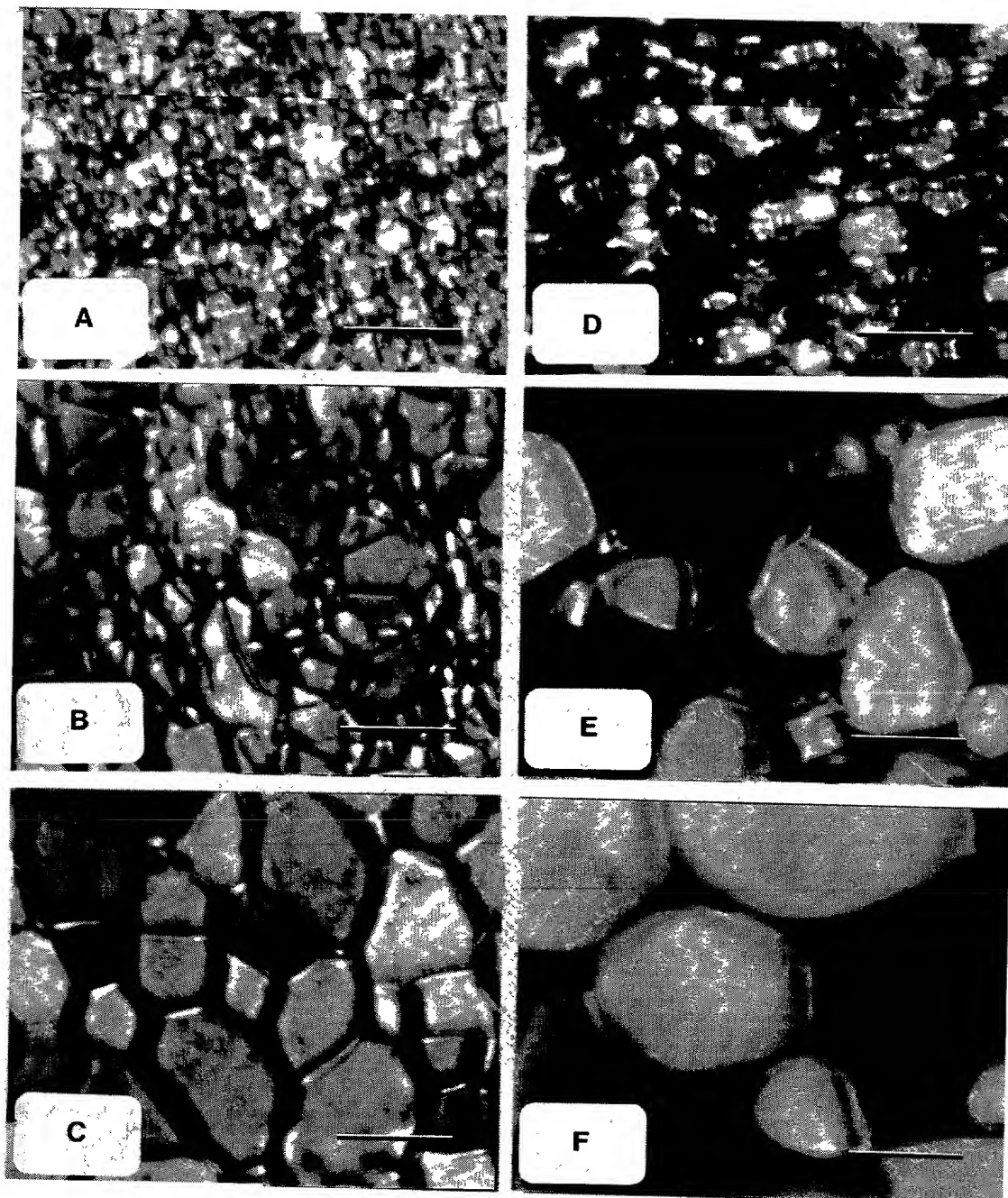


Fig. 8.0

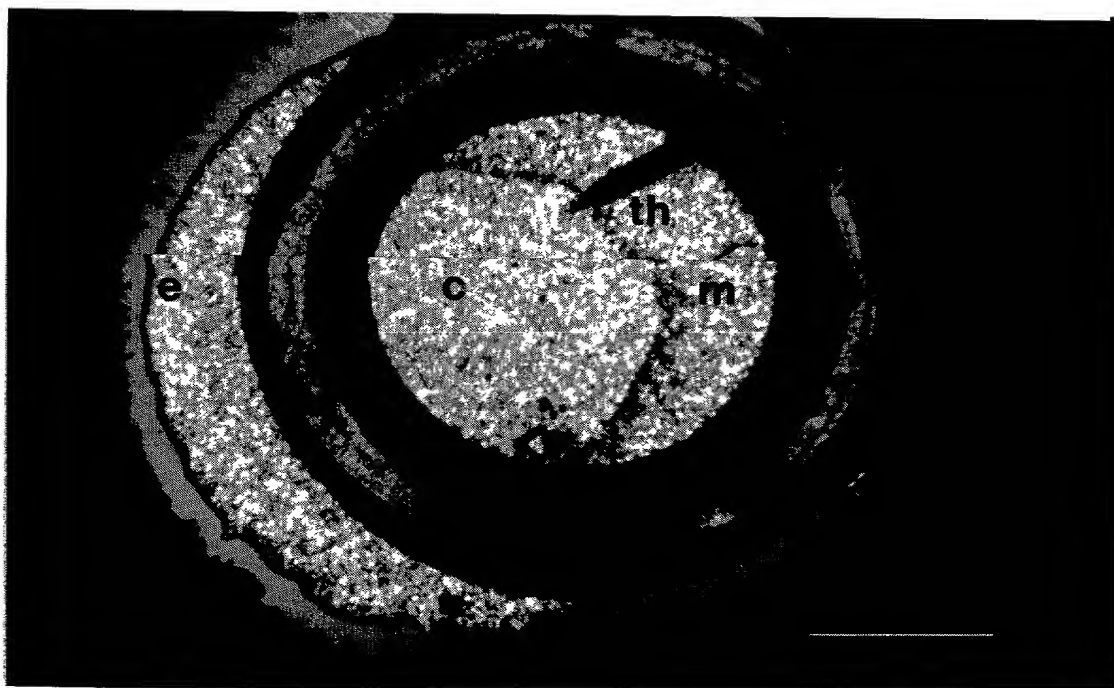


Fig. 8.1a

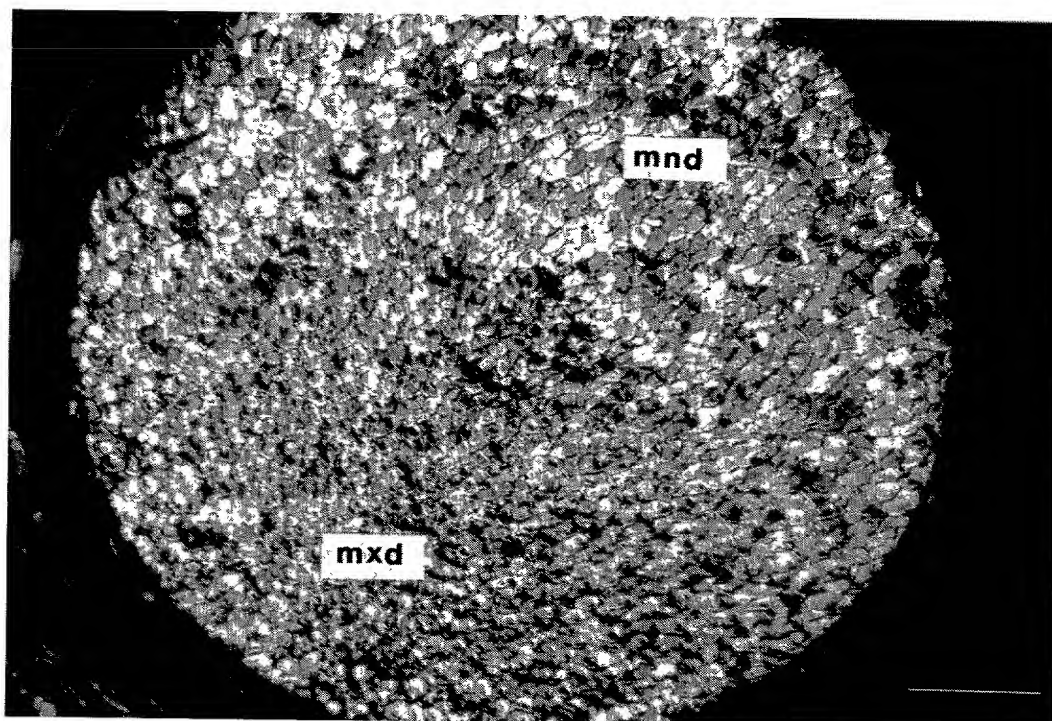
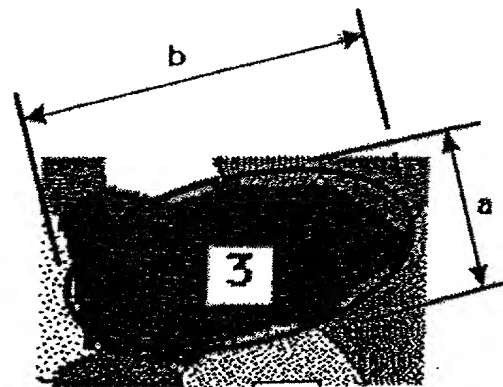
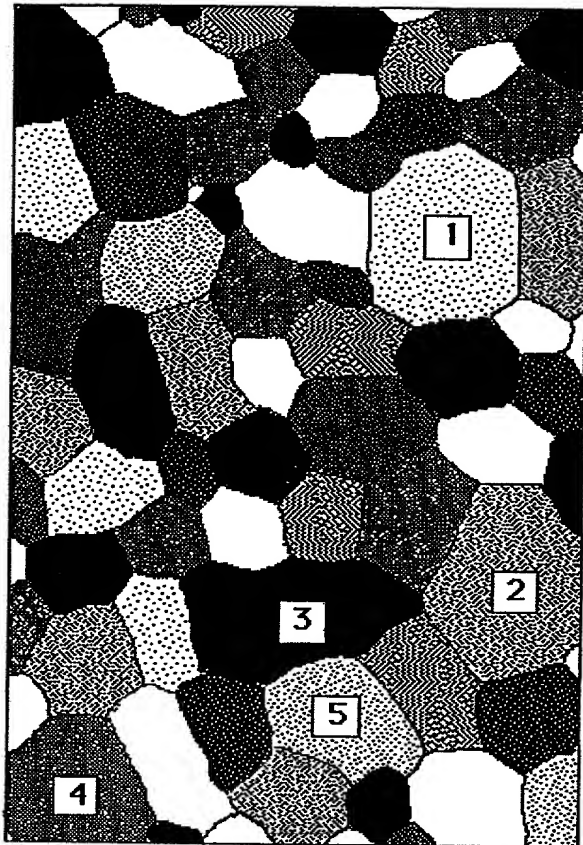


Fig. 8.1b



grain area = $0.25\pi ab$

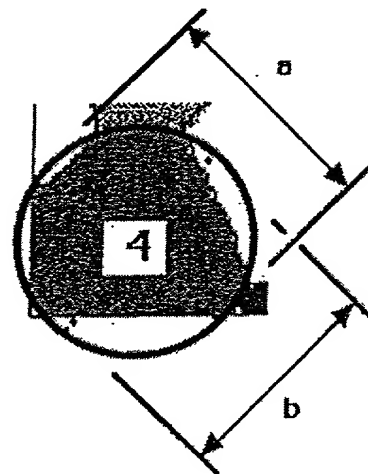


Fig. 8.2

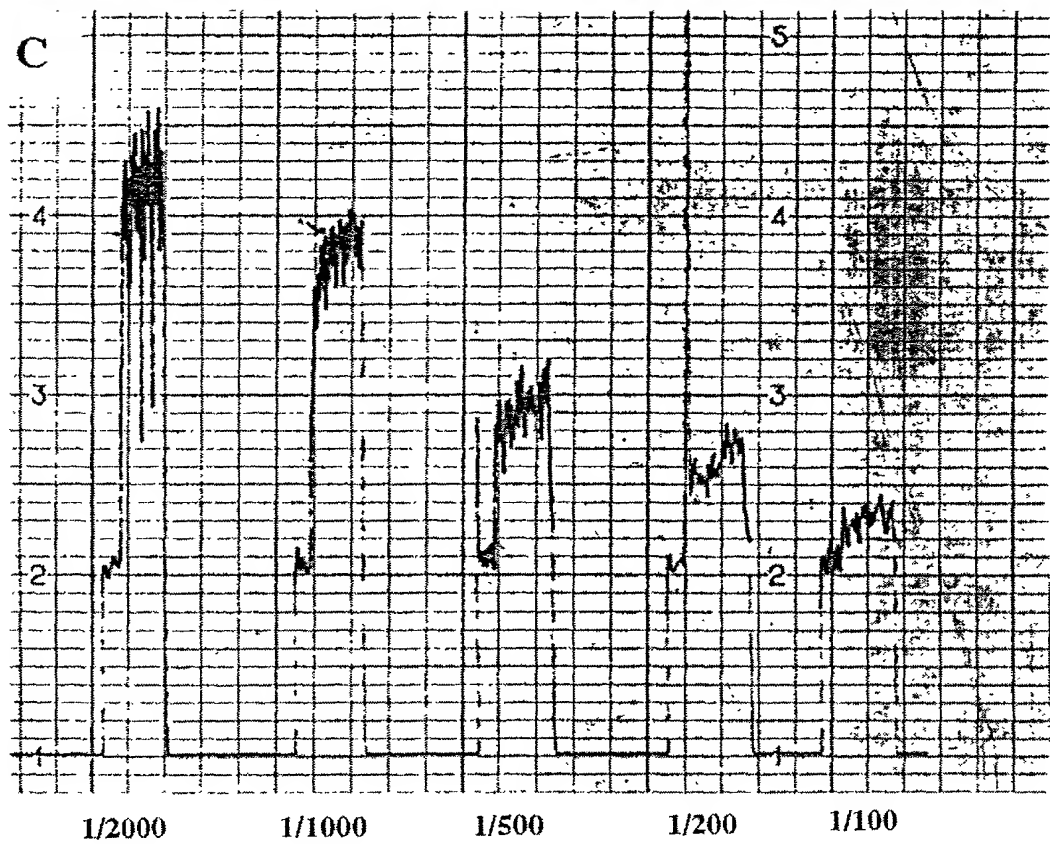
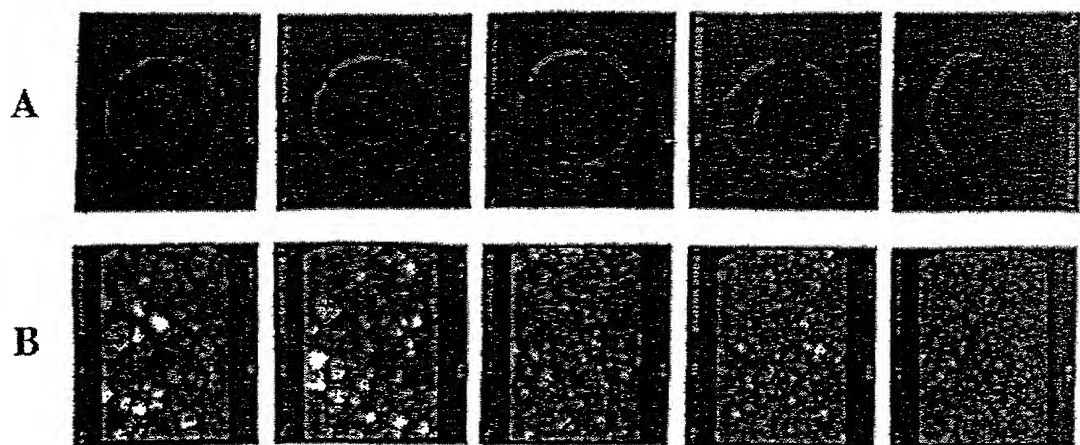


Fig. 8.3

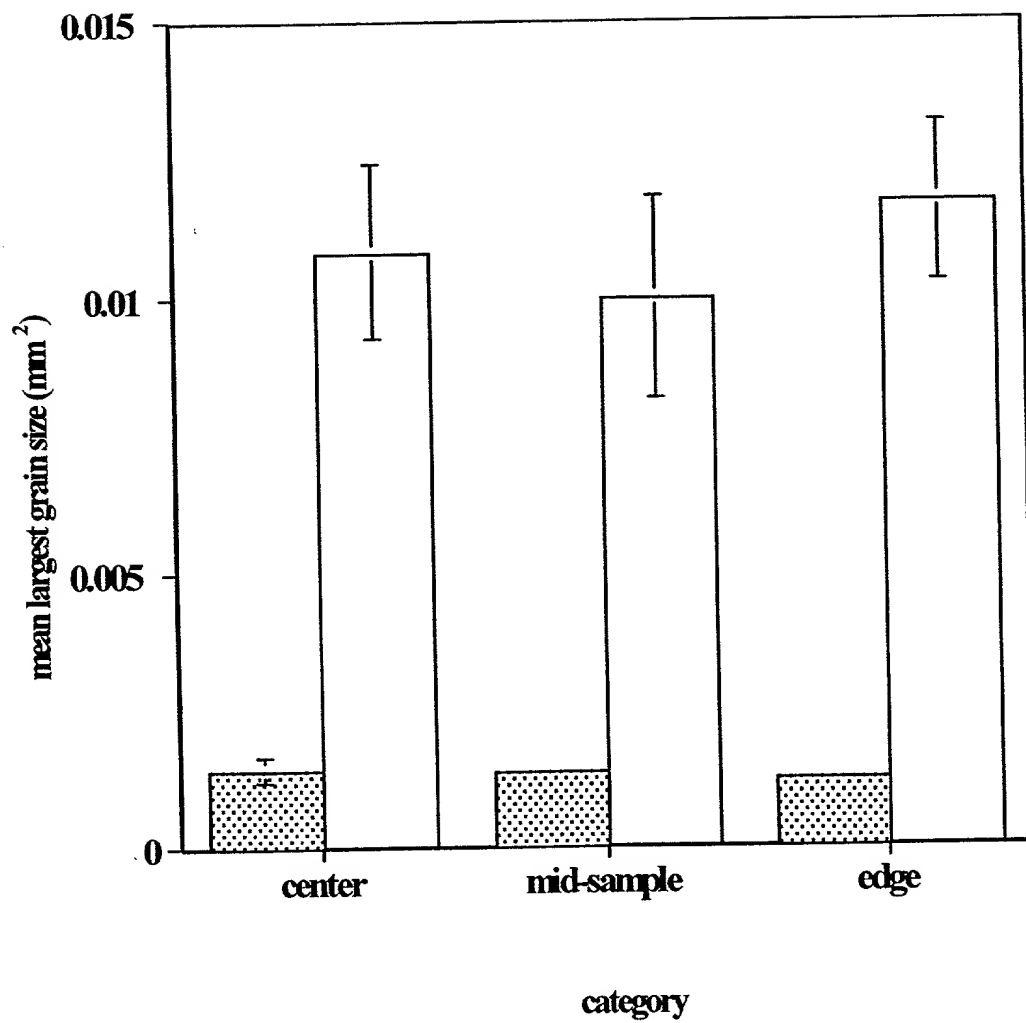


Fig. 8.4a

00076349, 012802

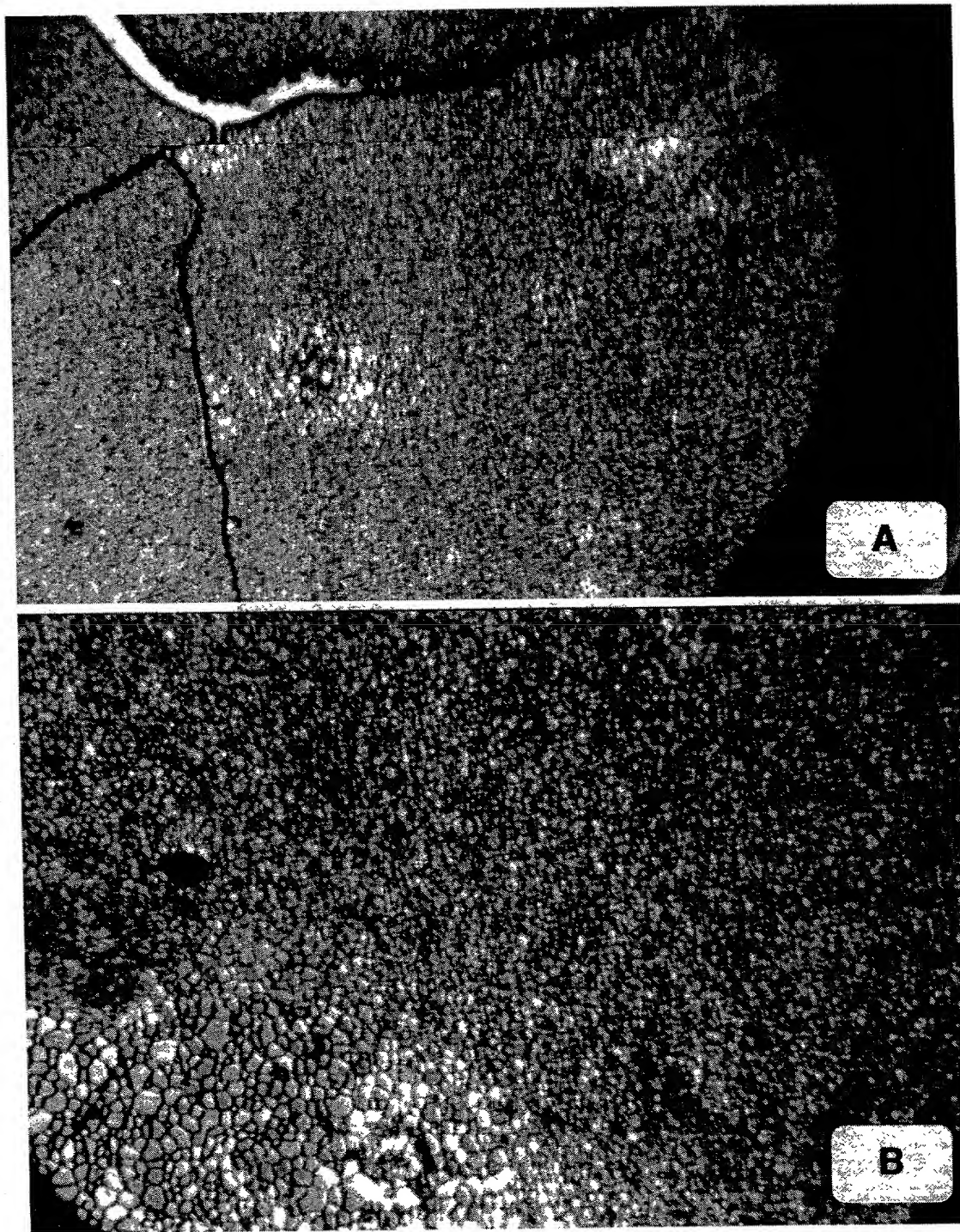


Fig. 8.46

202210 04E92860

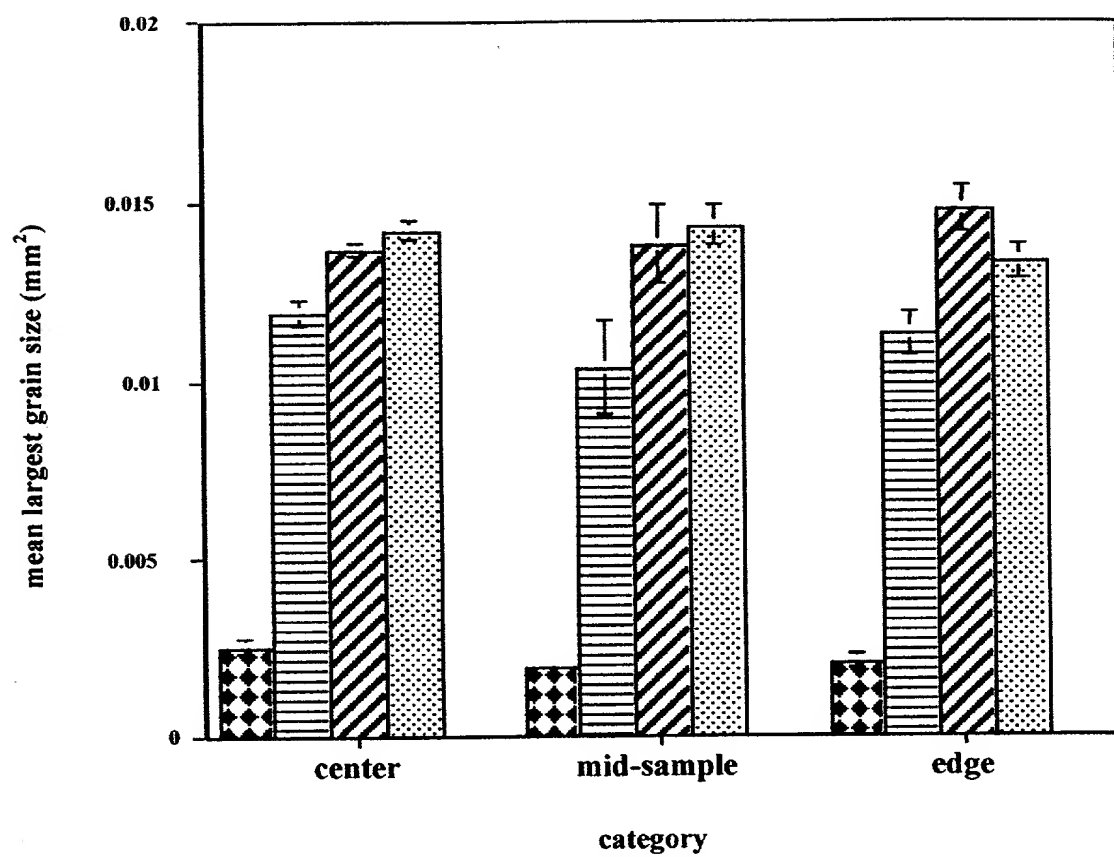


Fig. 8.5a

09876348-01302

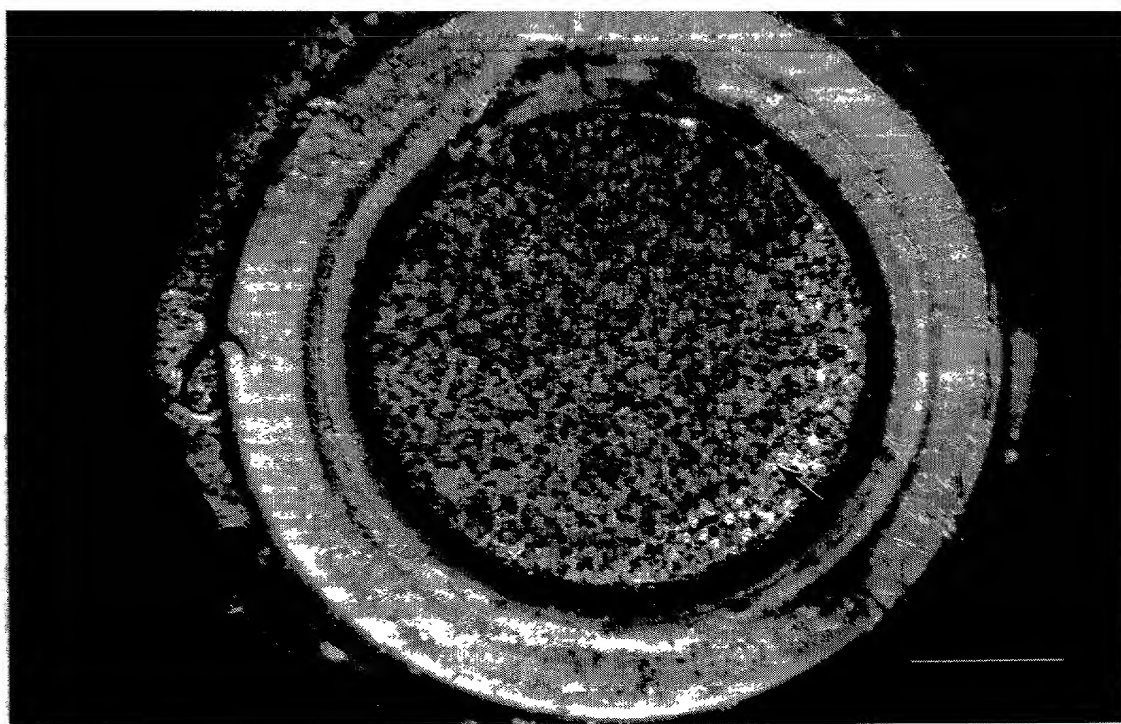


Fig. 8.5b

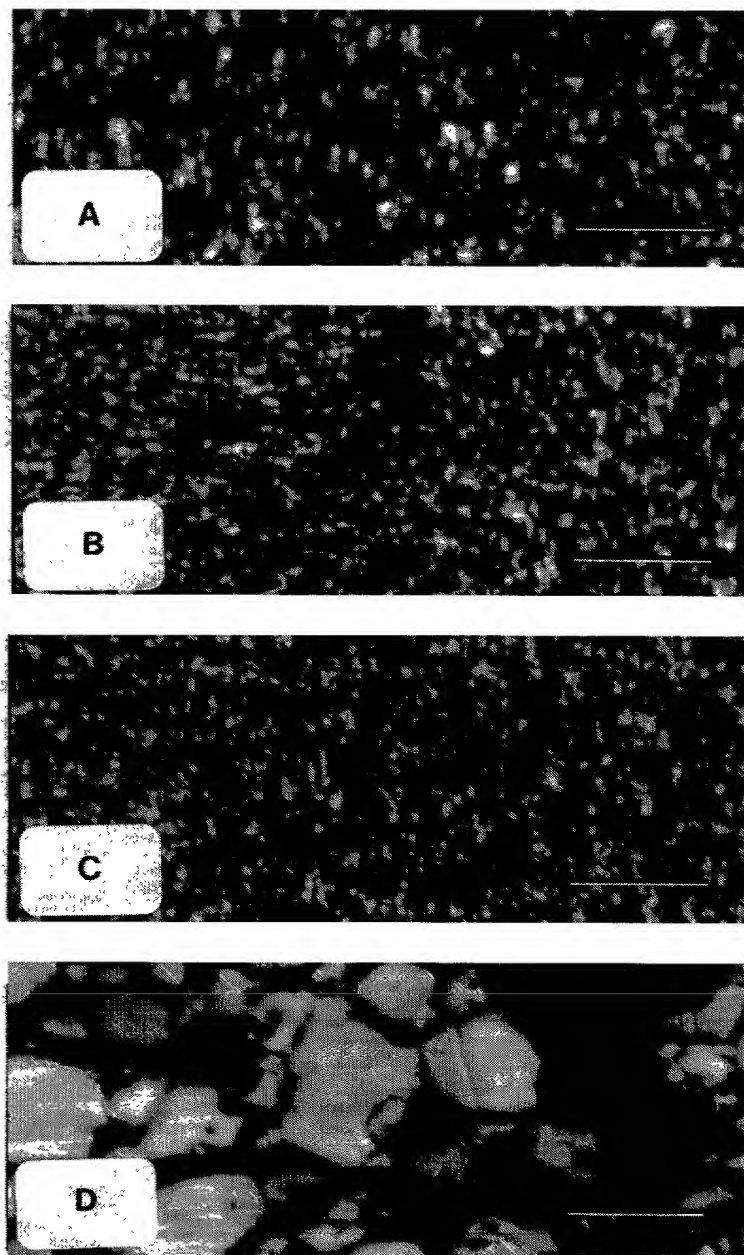


Fig. 8.6

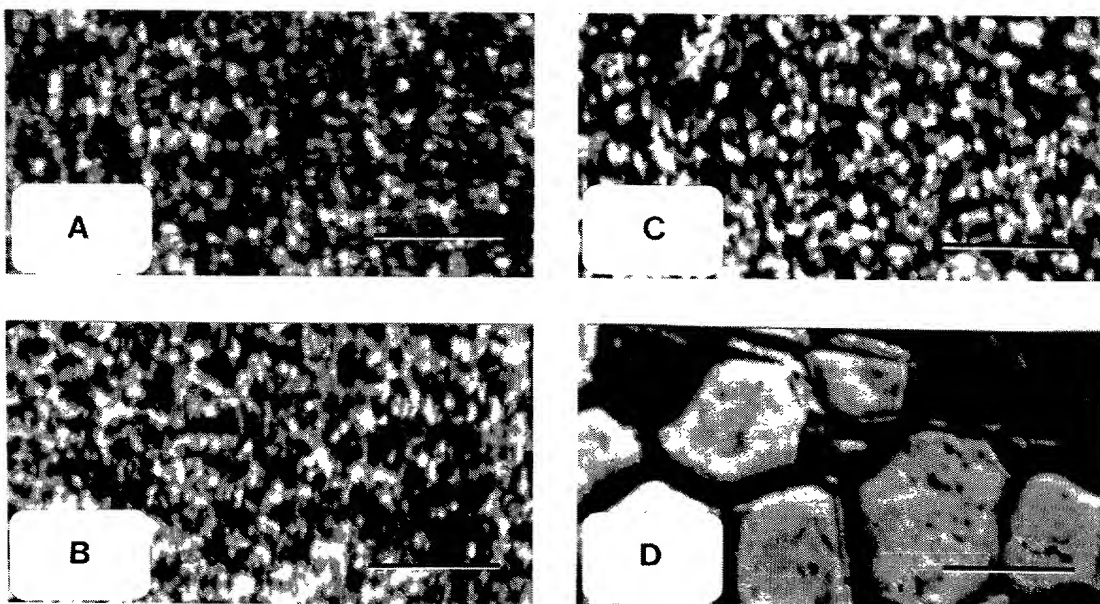
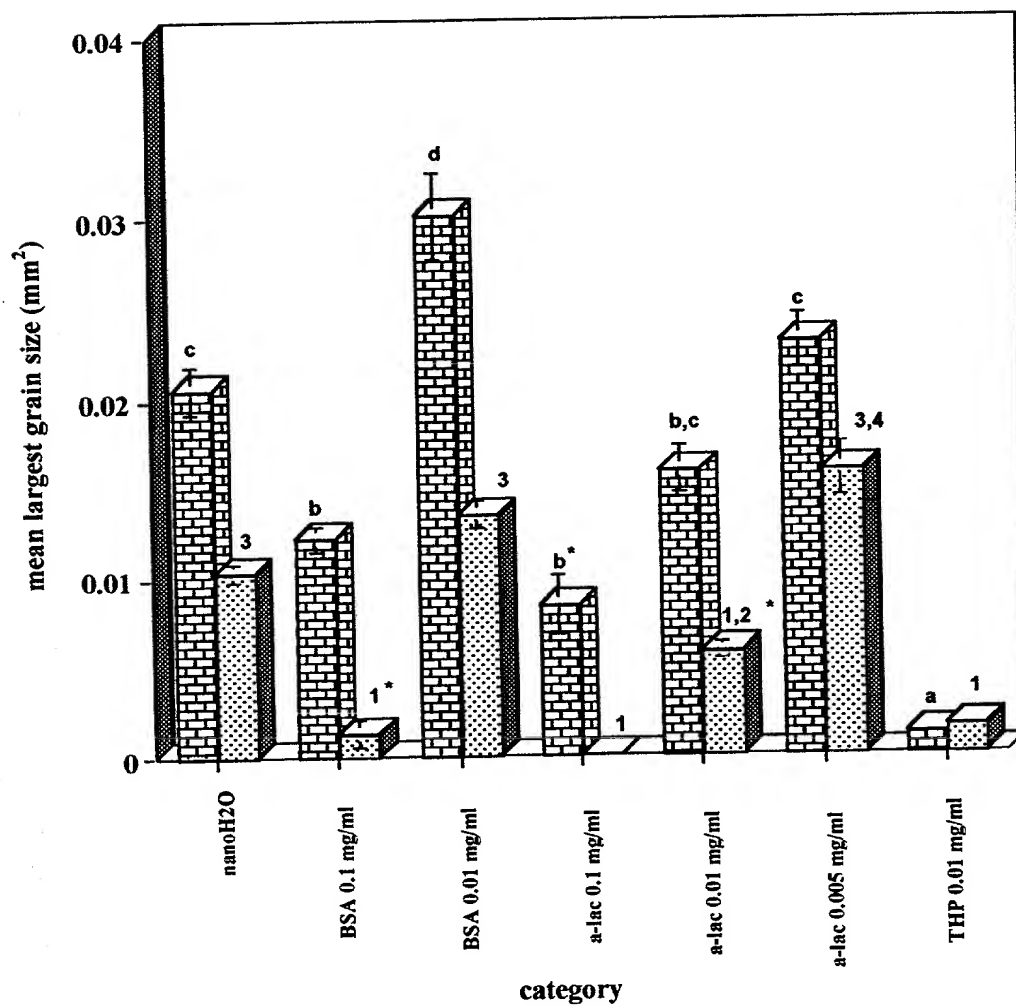


Fig. 8.7

*Fig. 8.8*

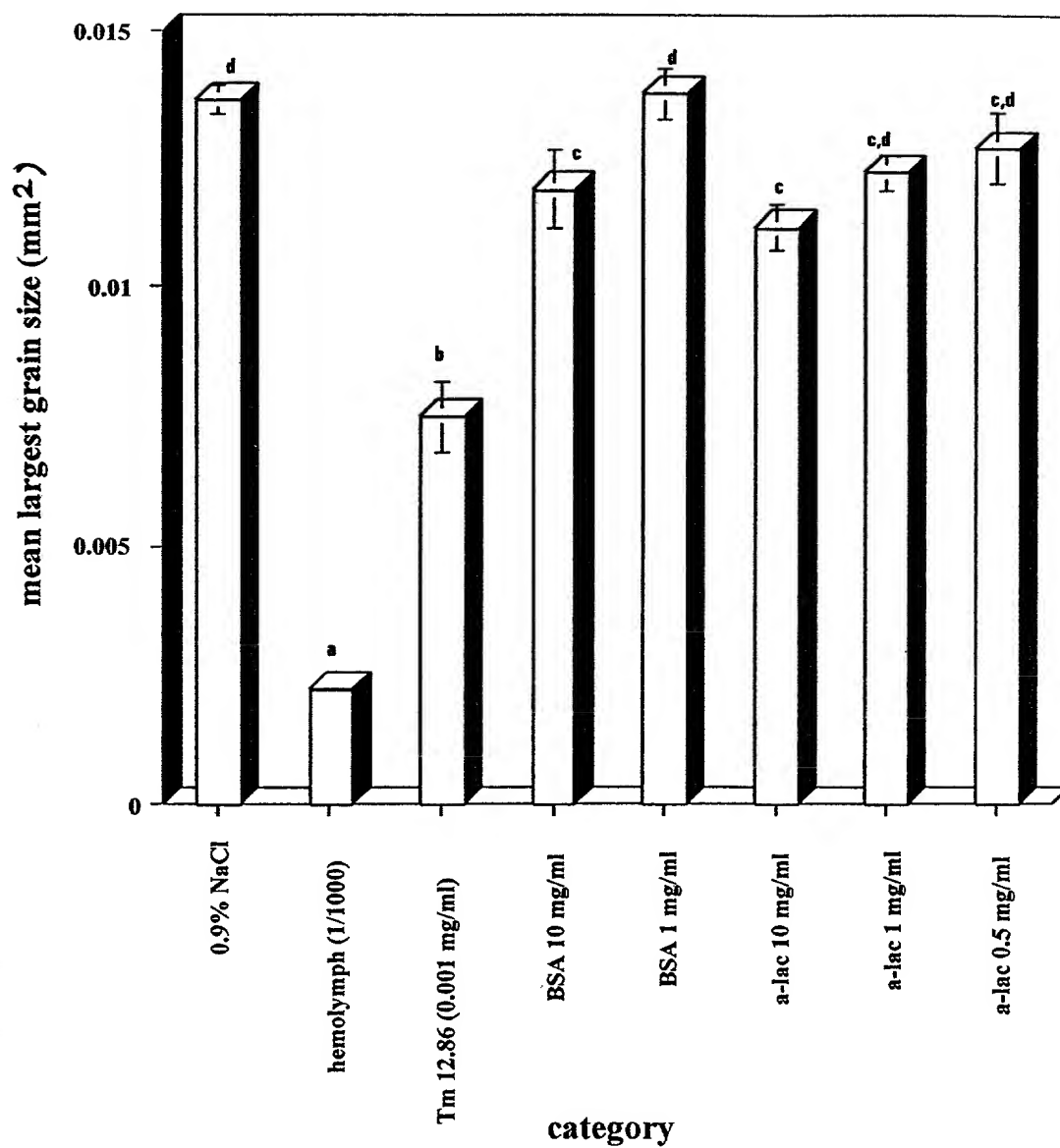


Fig. 8.9

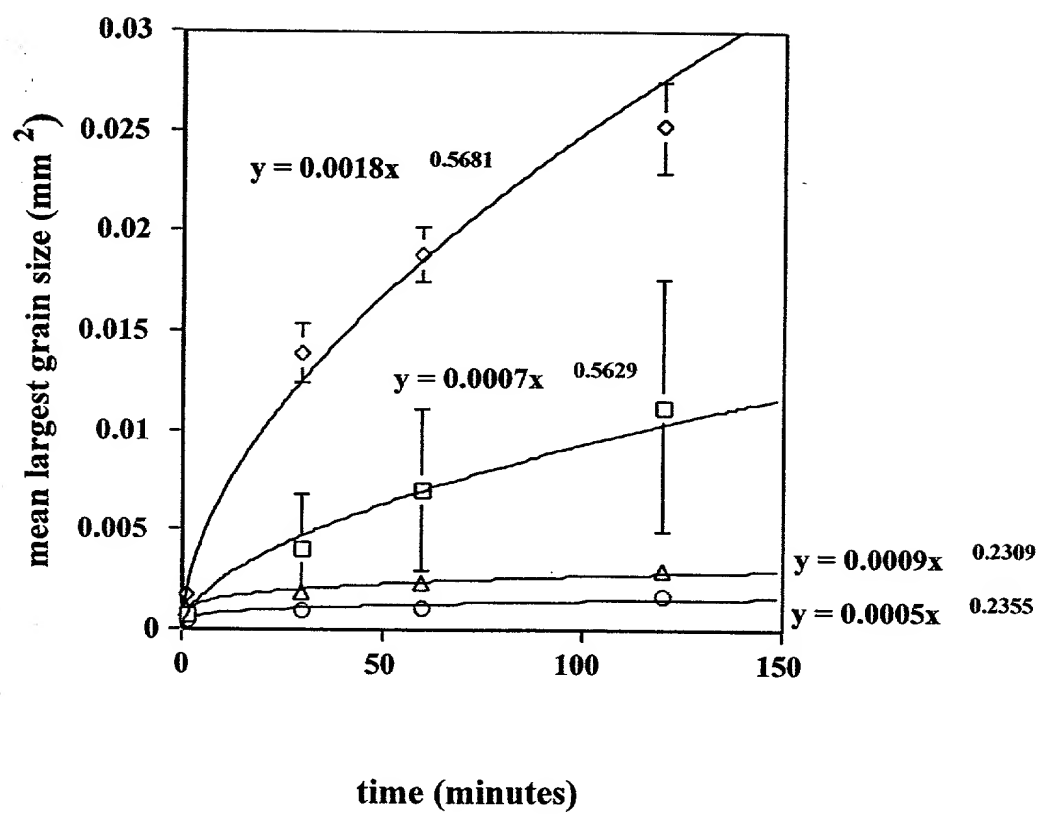


Fig. 8.10

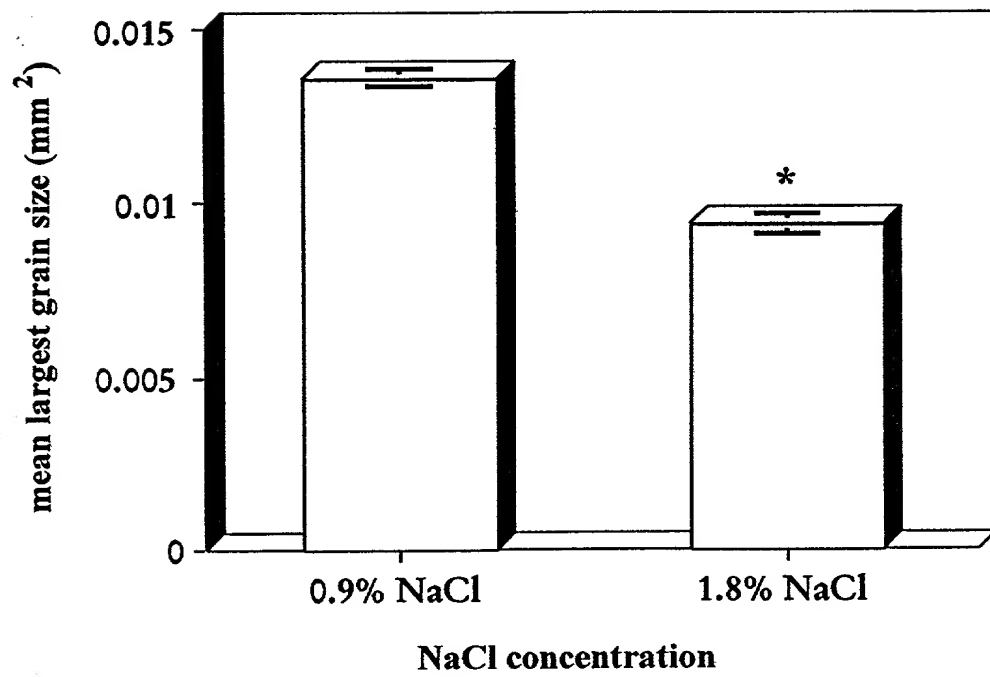


Fig. 8.11



Fig. 8.12

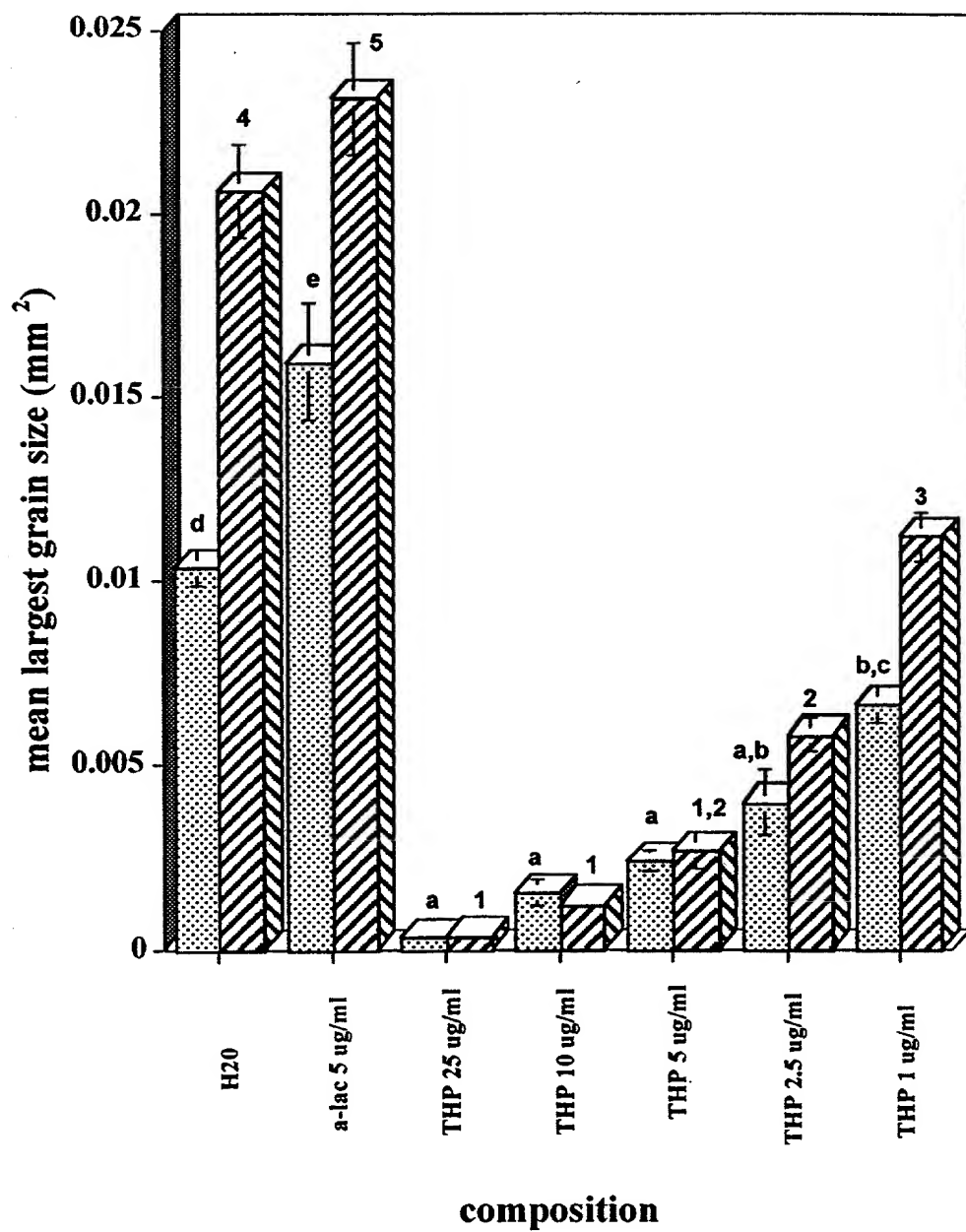


Fig. 8.13

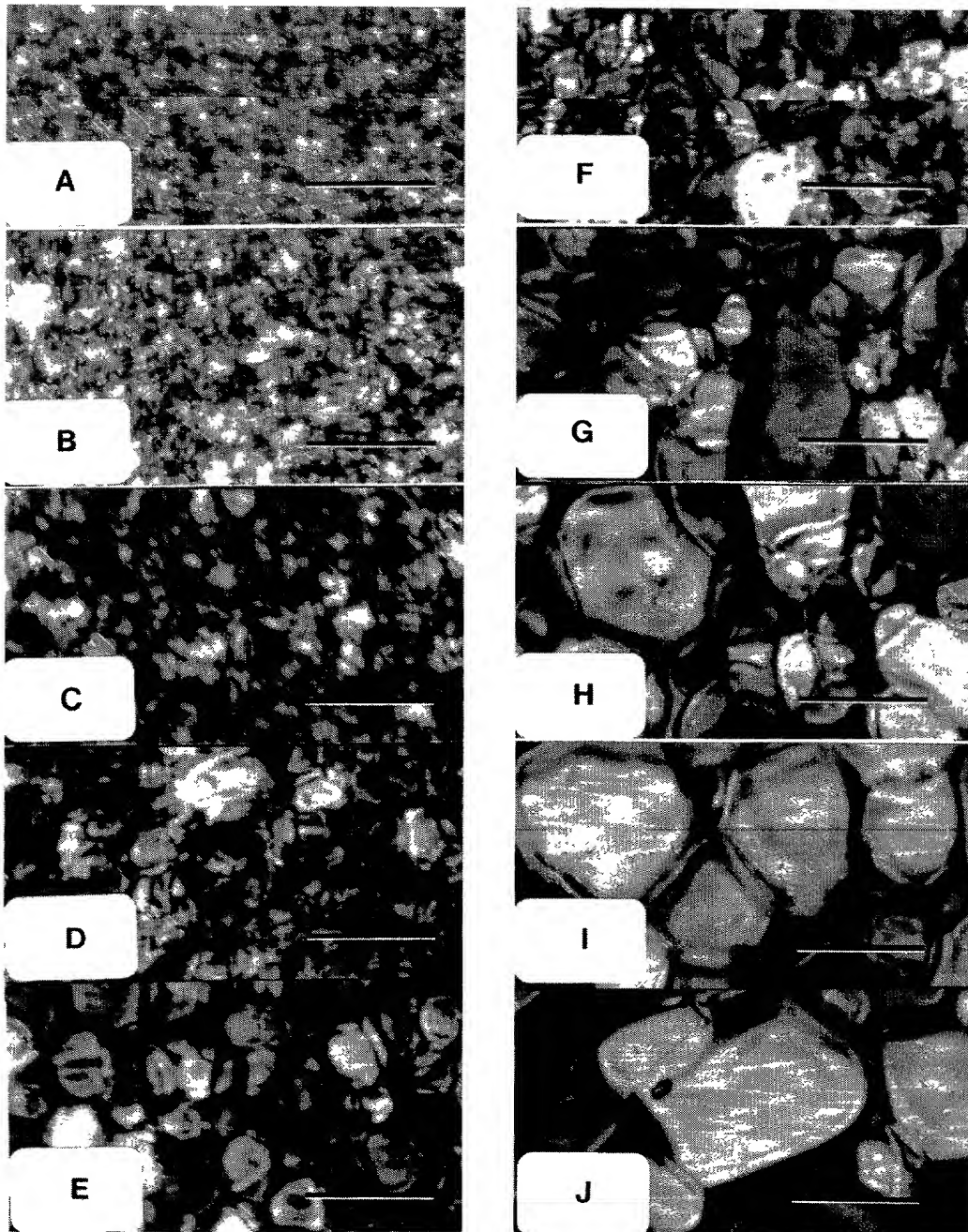


Fig. 8.14

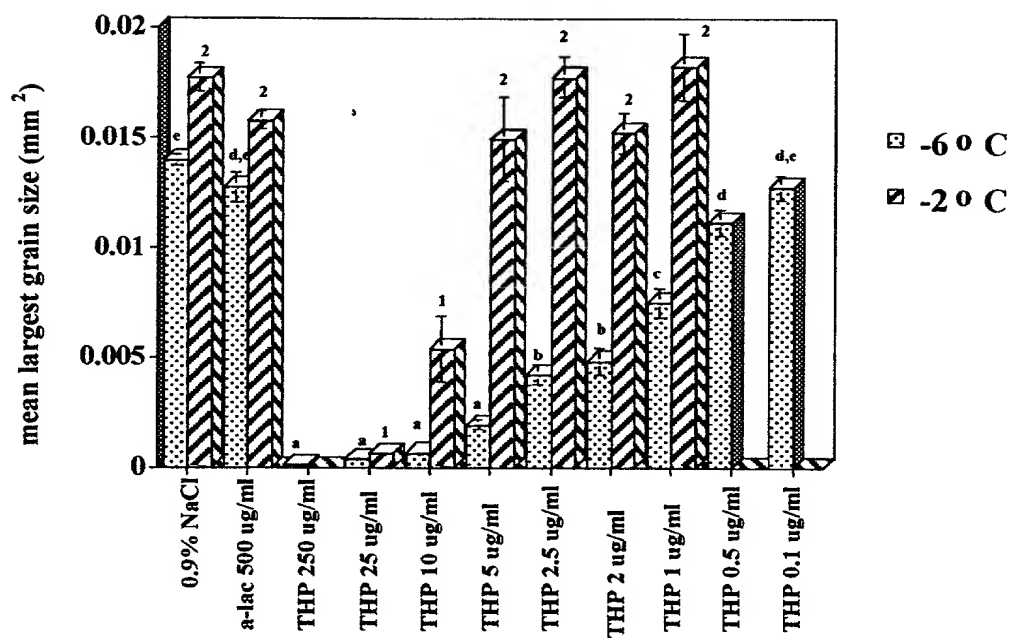


Fig. 8.15

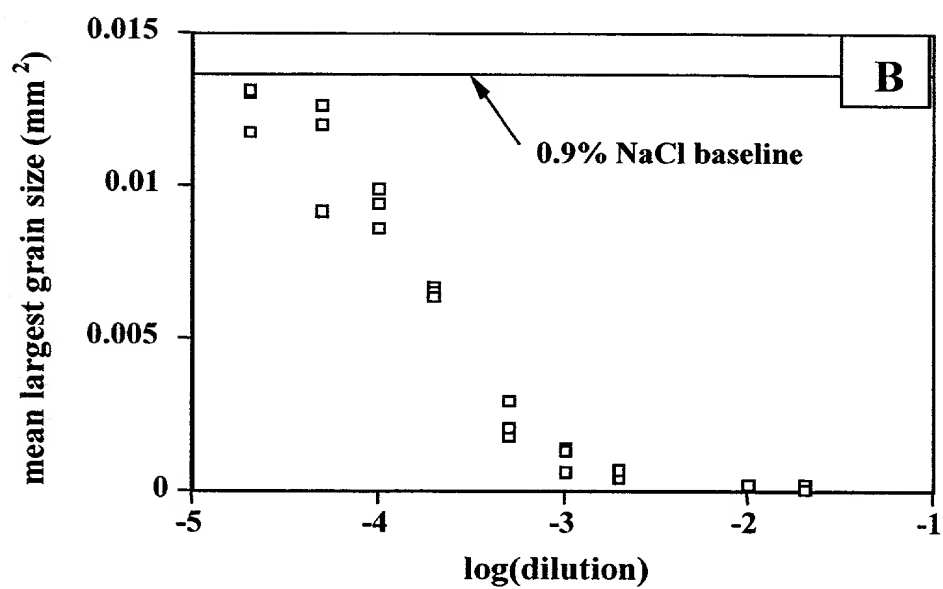
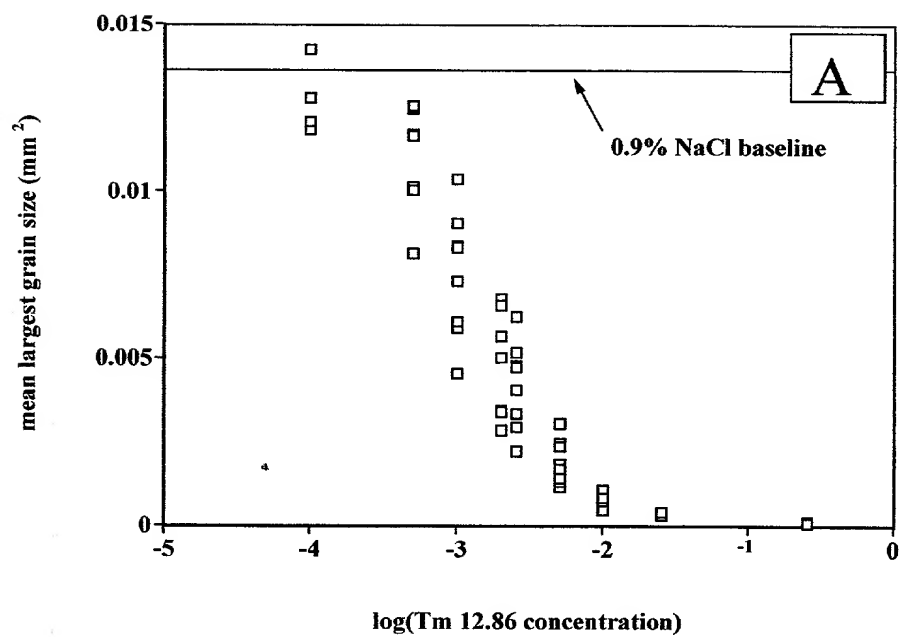


Fig. 8.16

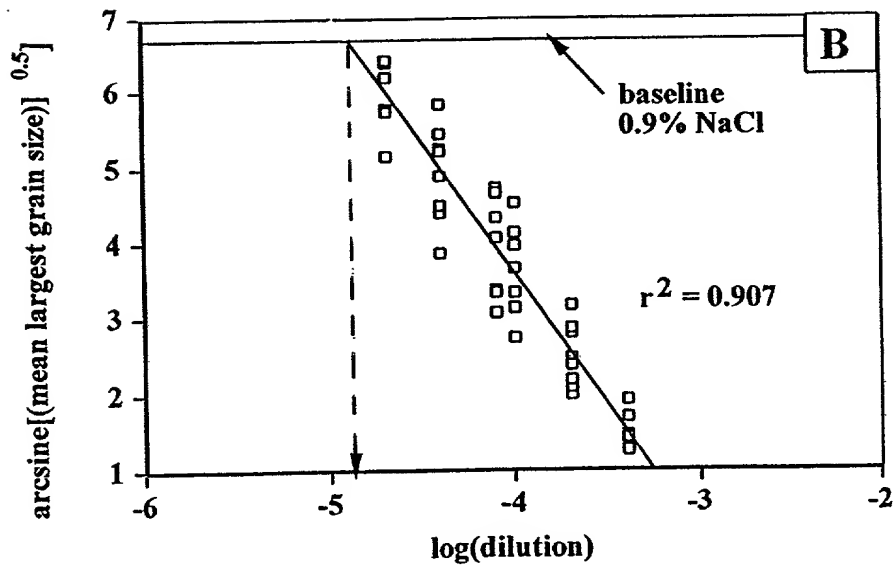
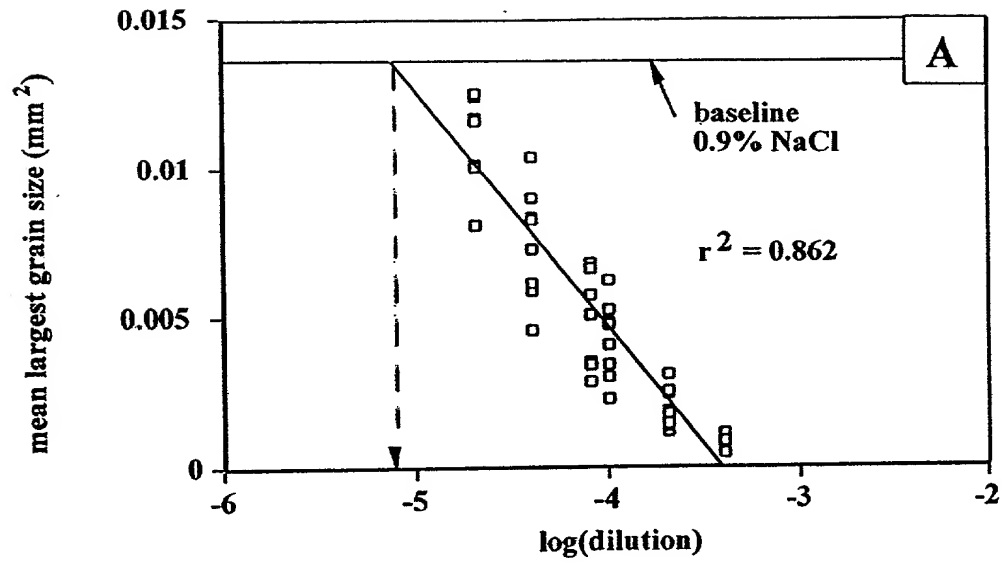


Fig. 8.17

202270 8149 250

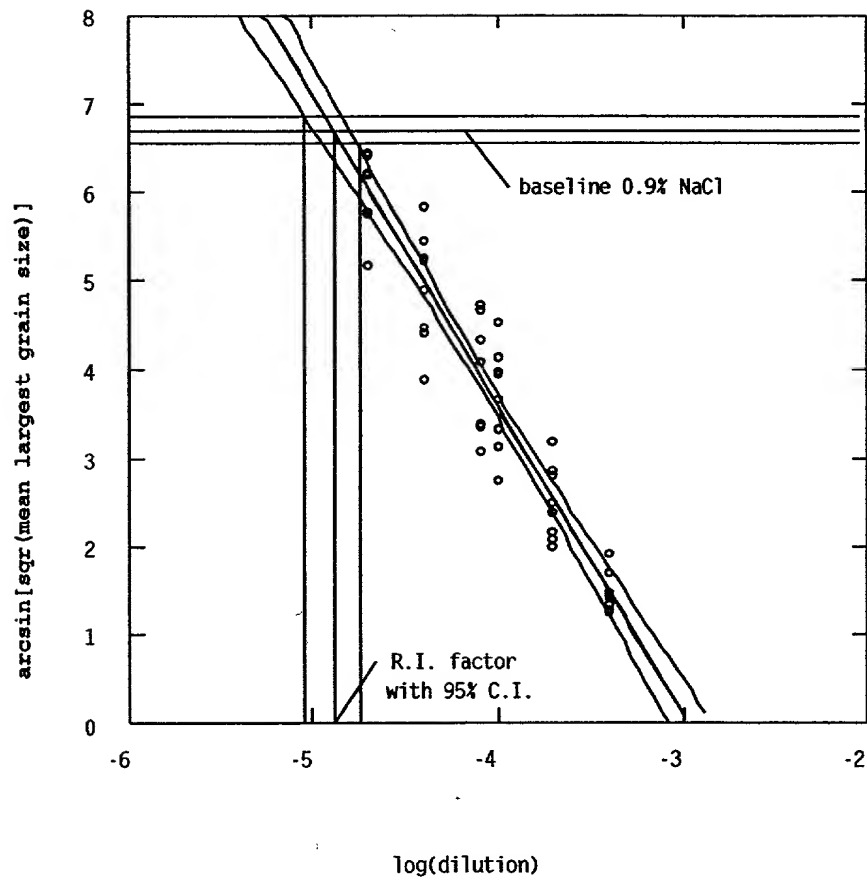


Fig. 8.18

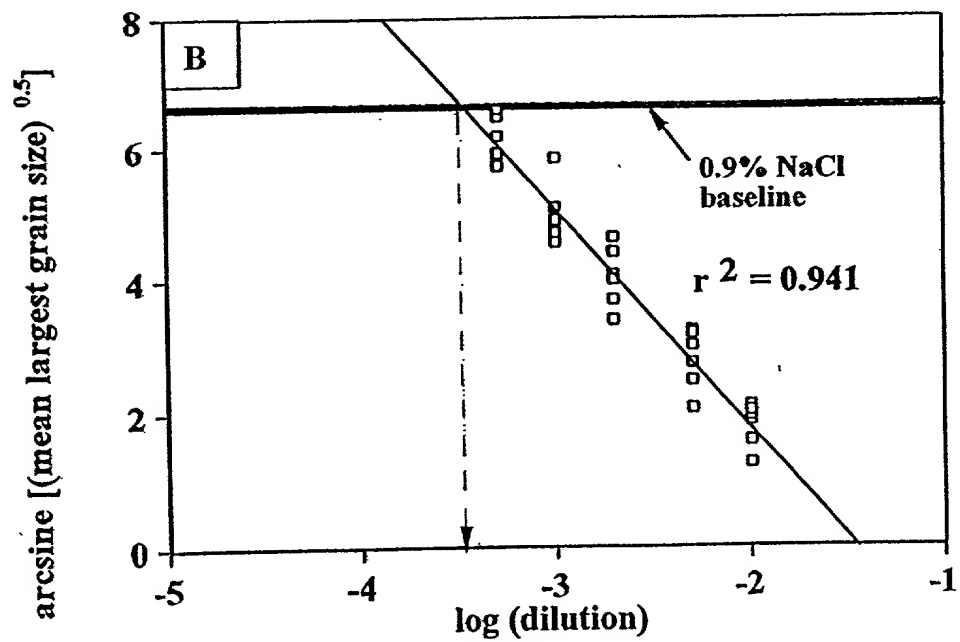
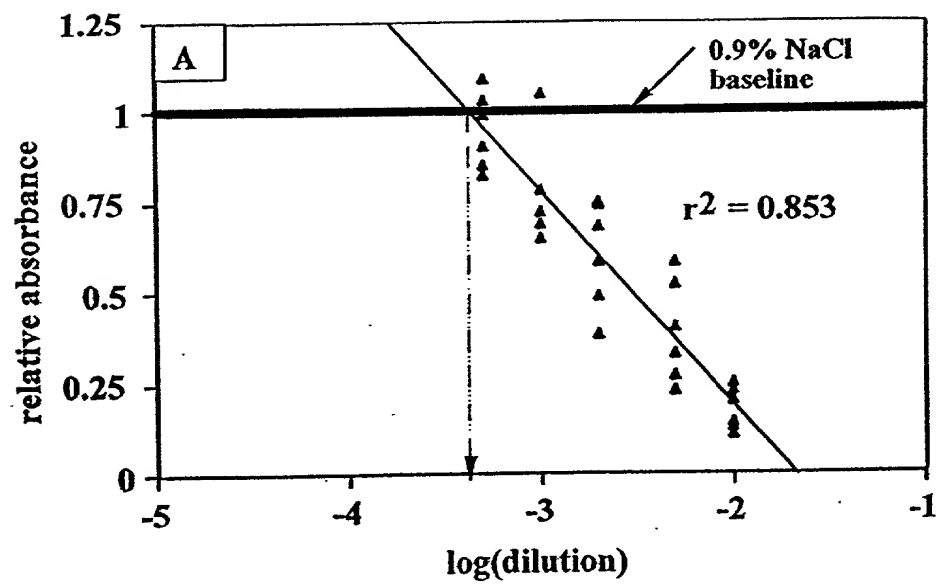


Fig. 8.19

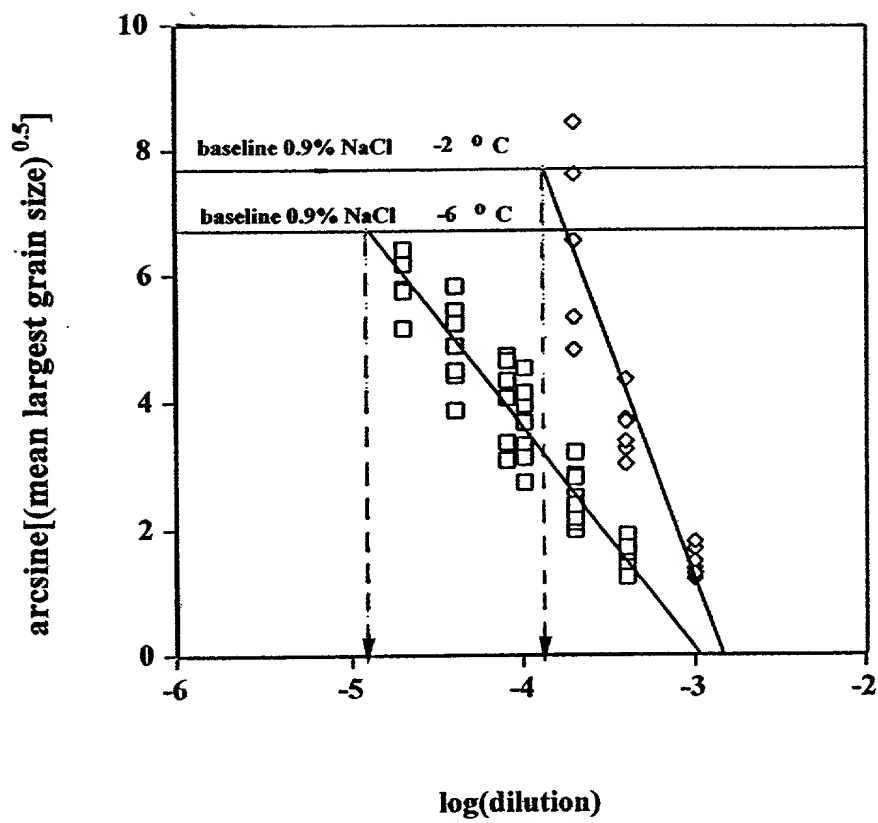


Fig. 8.20

208270-61E92860

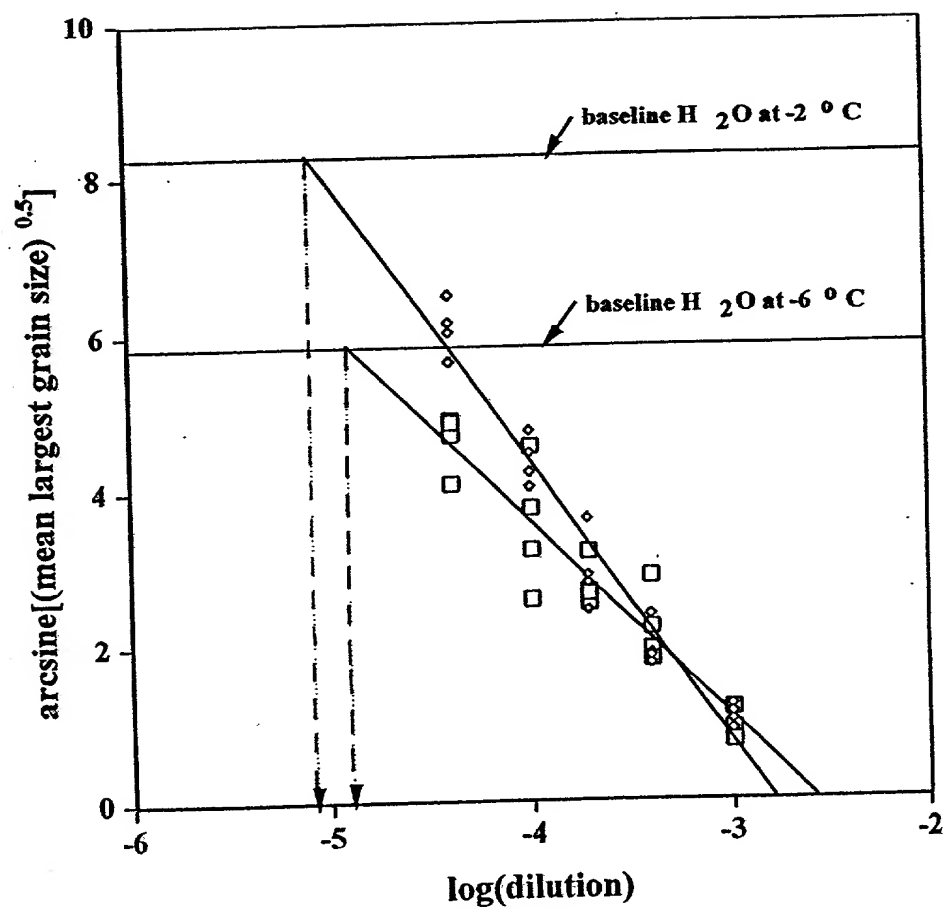


Fig. 8.21

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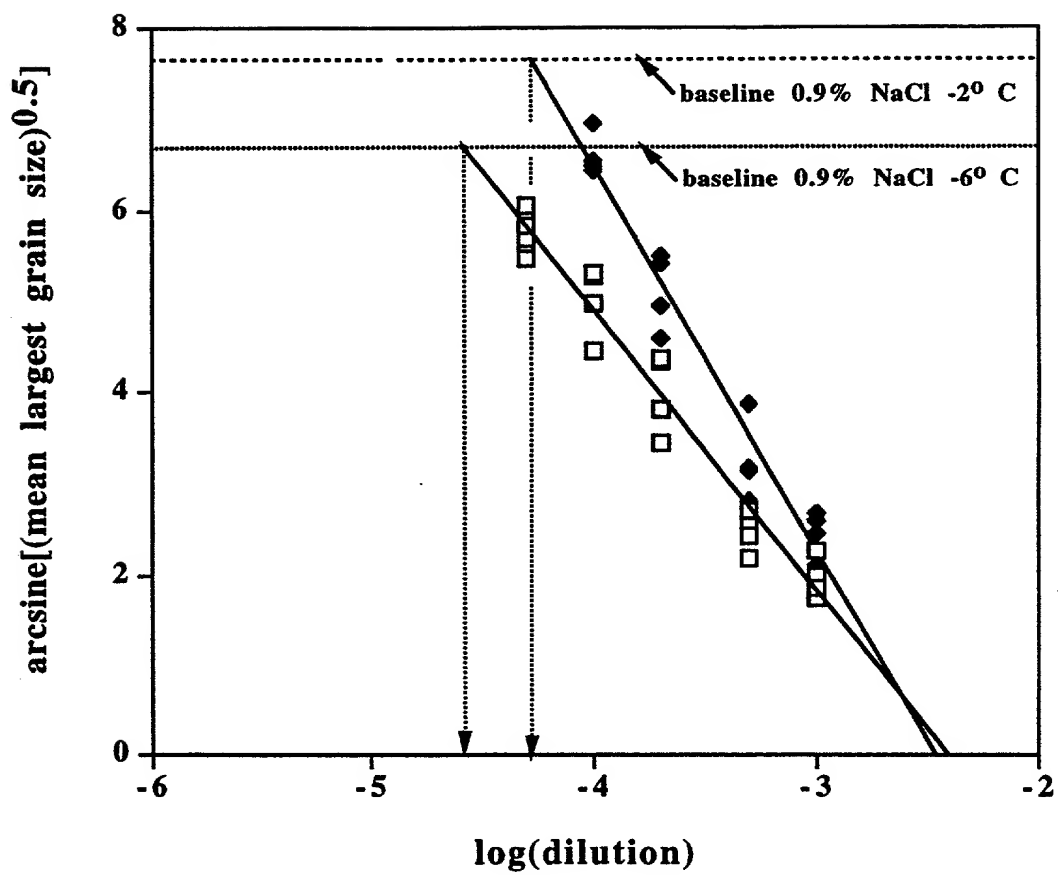


Fig. 8.22

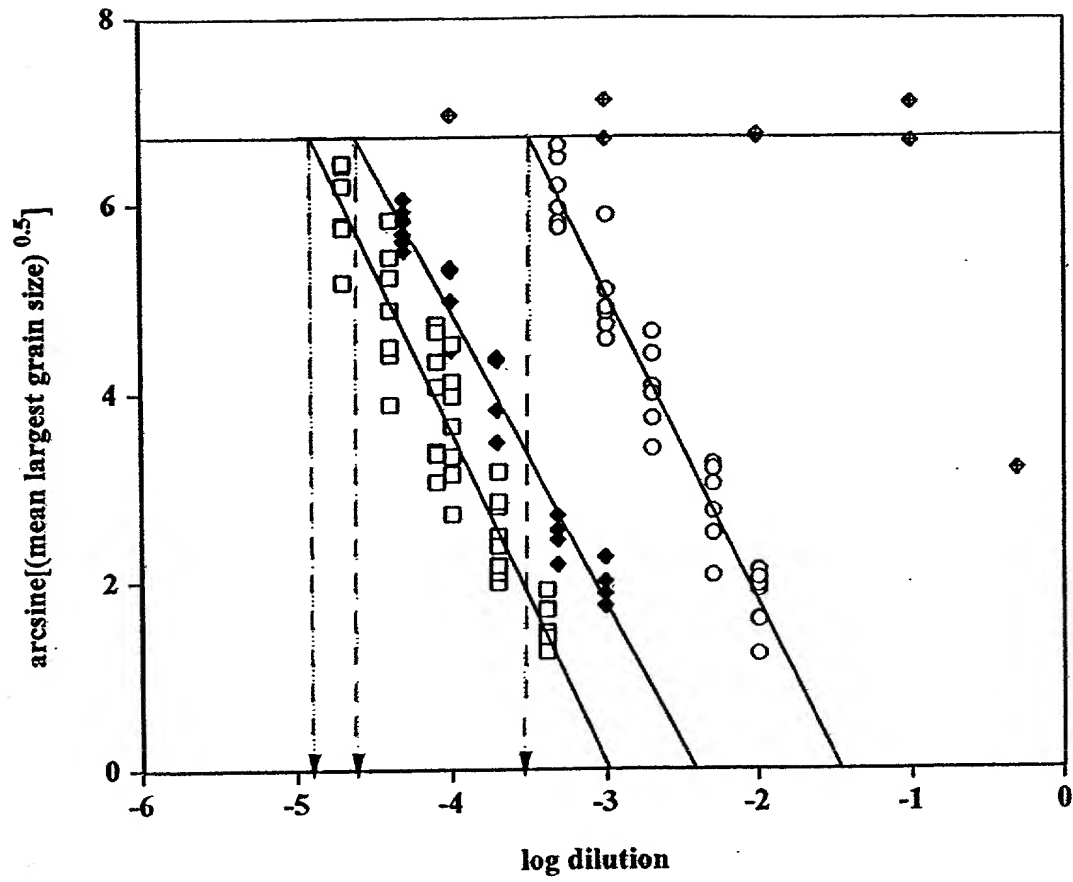


Fig. 8.23

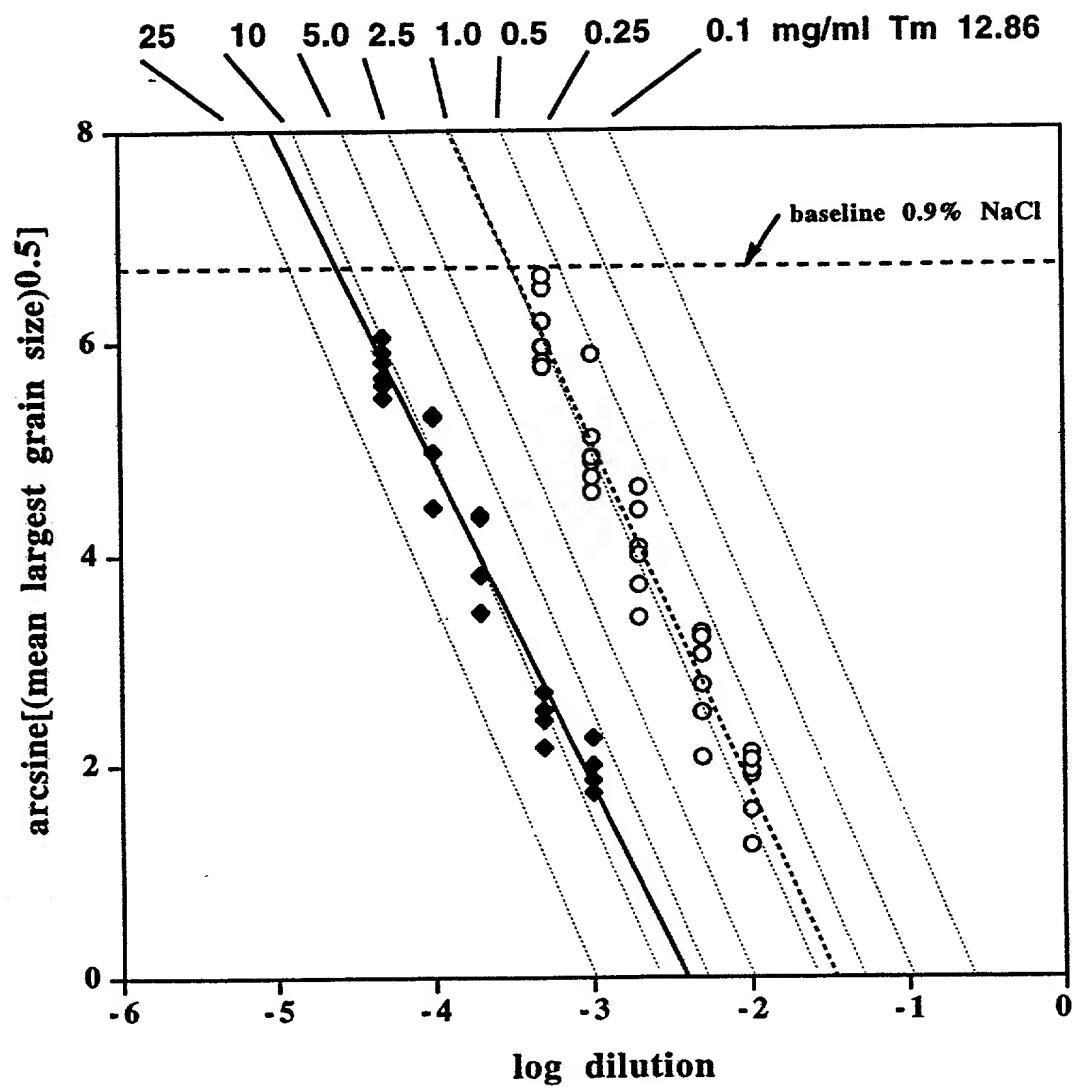


Fig. 8.24

202210-84E92860

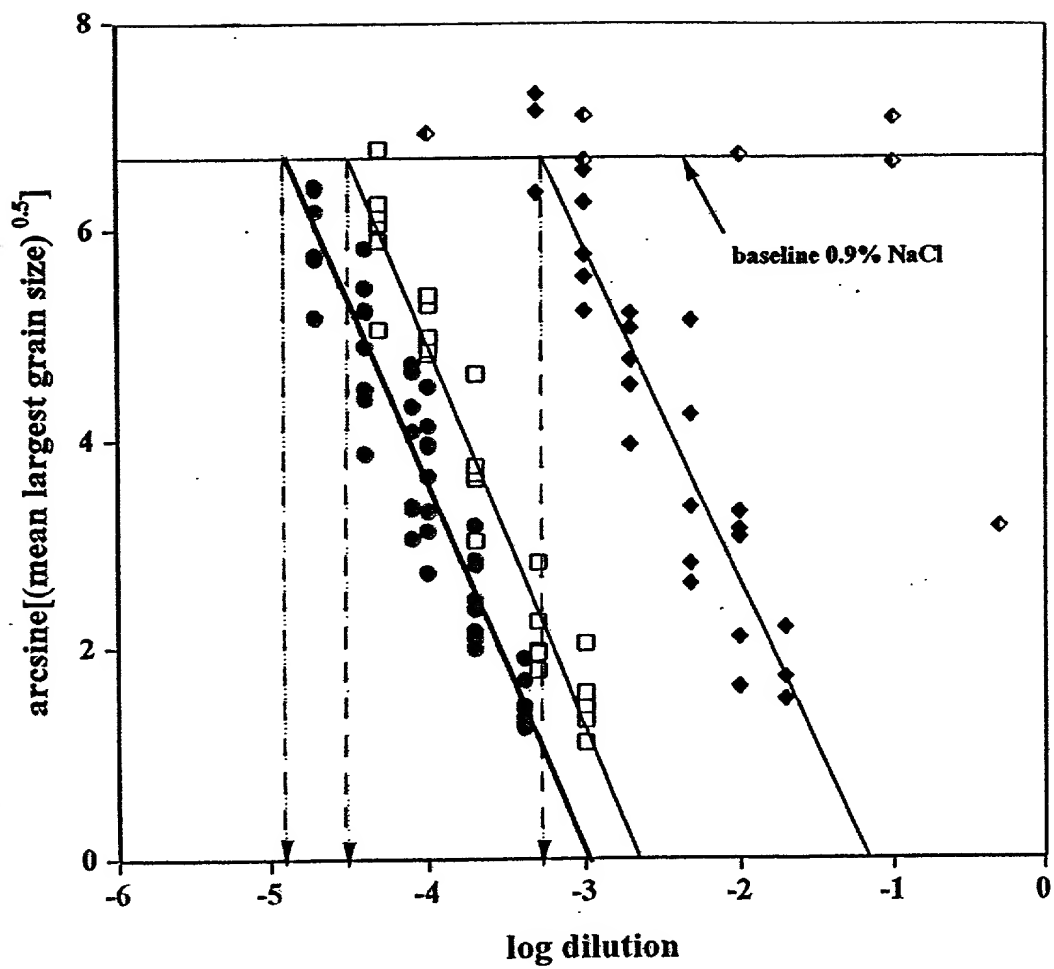


Fig. 8.25

208270* B1E92B6D

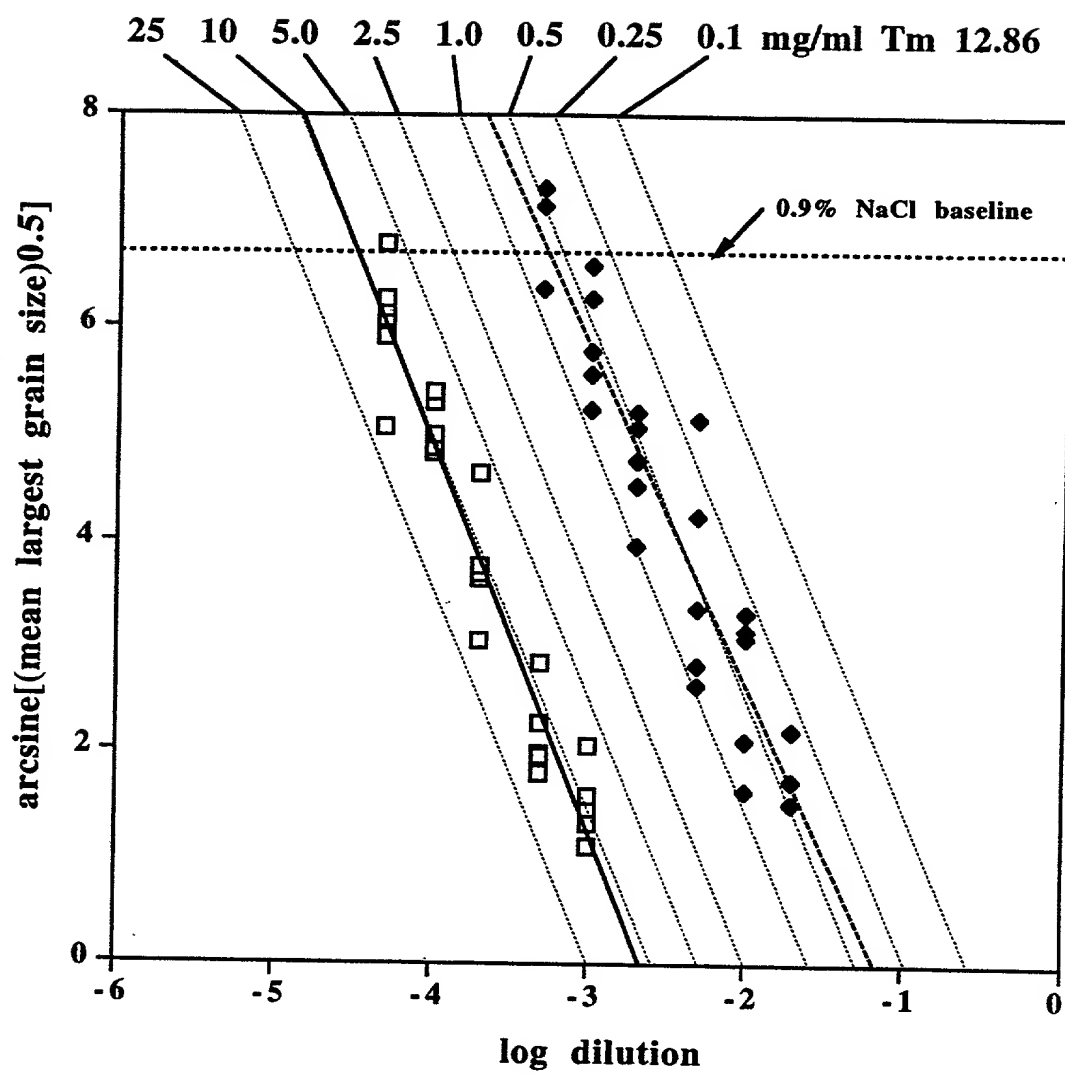


Fig. 8.26

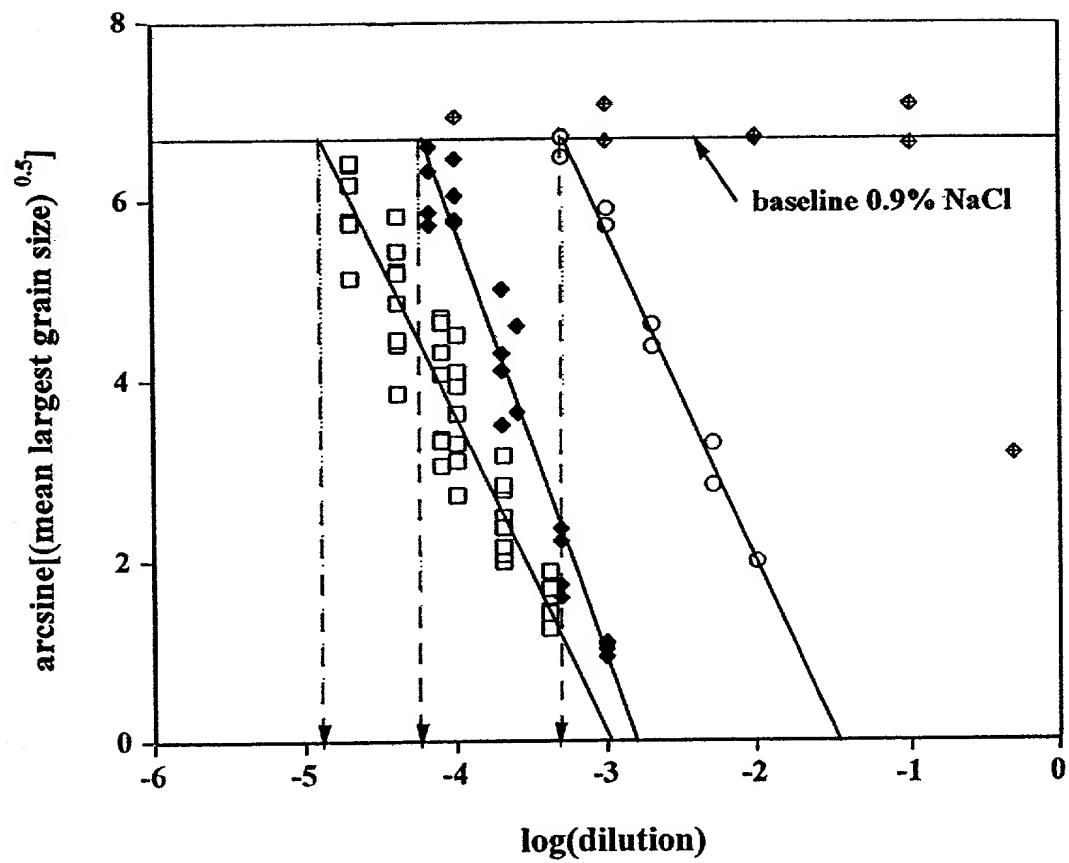
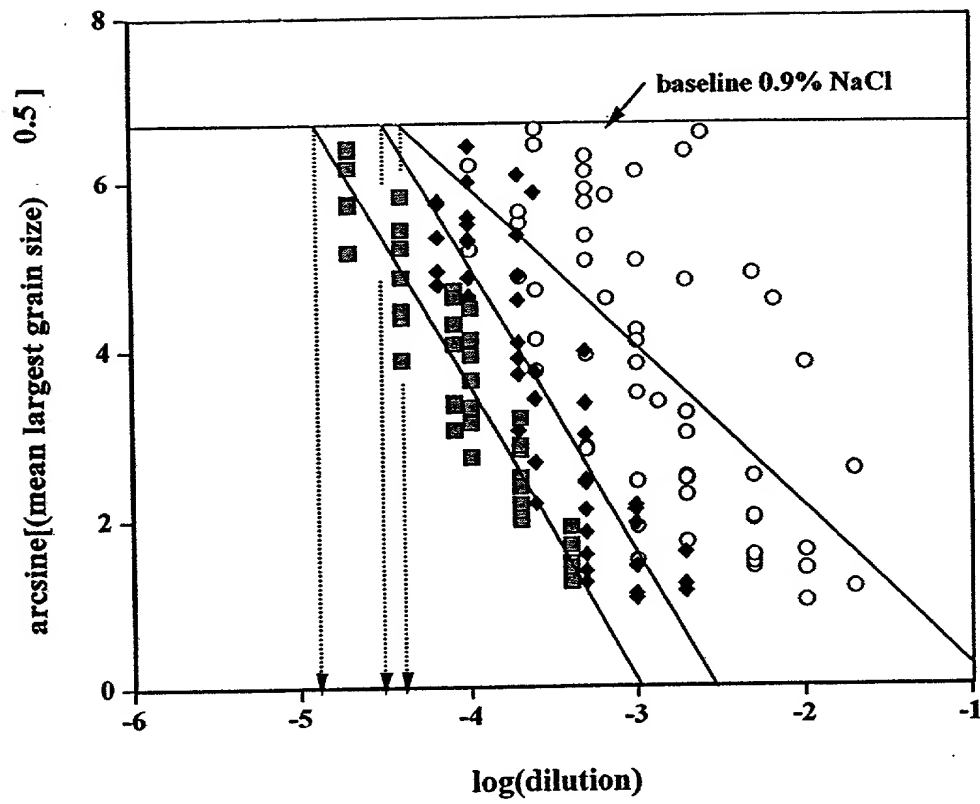


Fig. 8.27

*Fig. 8.28*

202210 04:59:28

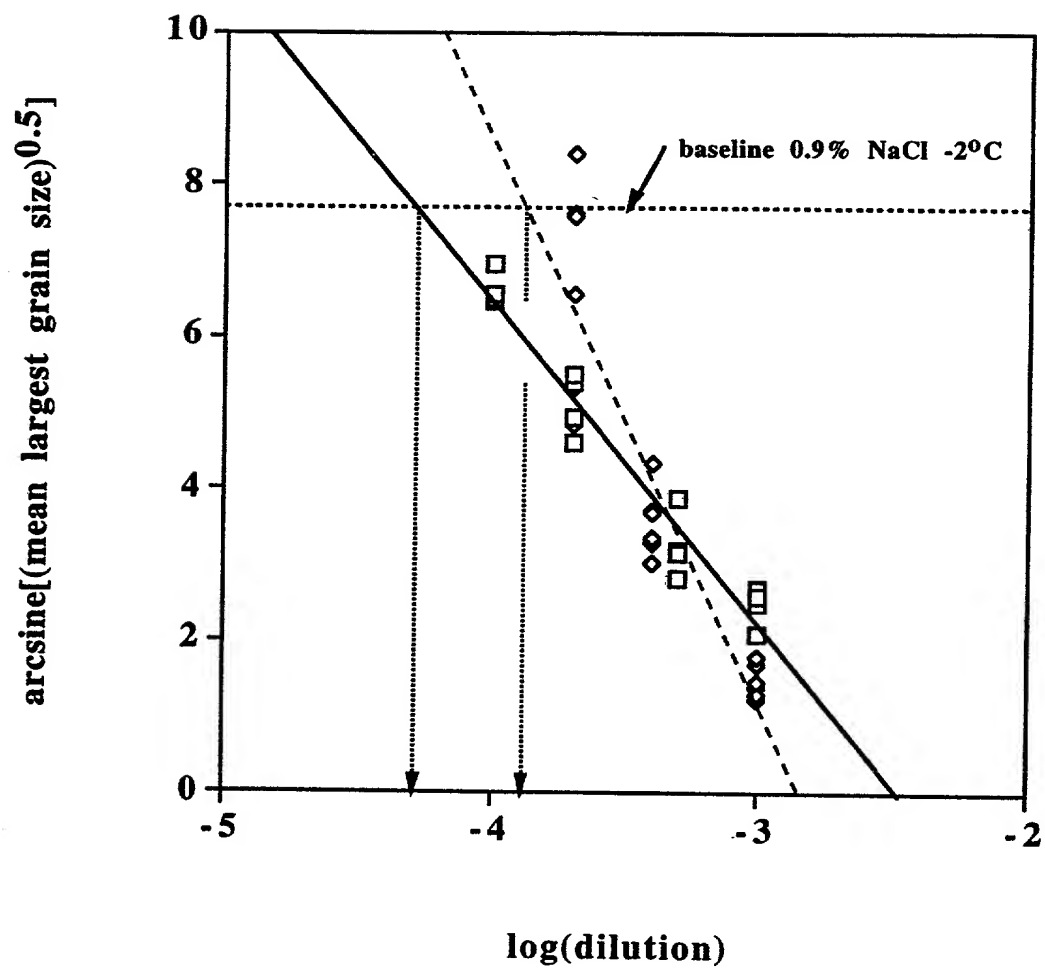


Fig. 8.29

Figure 1 is a scatter plot with three data series and three linear regression lines. The y-axis is labeled $\arcsine[(\text{mean largest grain size})^{0.5}]$ and ranges from 0 to 8. The x-axis is labeled $\log(\text{dilution})$ and ranges from -6 to 1. A horizontal line at $y \approx 6.7$ is labeled 'baseline 0.9% NaCl'. The data series are represented by open circles, open squares, and open diamonds. Each series has a corresponding linear regression line that changes slope at specific $\log(\text{dilution})$ values, marked by vertical dashed lines at approximately -5.0, -3.4, and -1.8. The slopes of the regression lines are steepest for the diamond series and shallowest for the circle series.

$\log(\text{dilution})$	$\arcsine[(\text{mean largest grain size})^{0.5}]$ (Circles)	$\arcsine[(\text{mean largest grain size})^{0.5}]$ (Squares)	$\arcsine[(\text{mean largest grain size})^{0.5}]$ (Diamonds)
-4.8	5.5		
-4.6	5.6		
-4.4	4.5		
-4.2	4.7		
-4.0	4.6		
-3.8	3.4		
-3.6	3.2		
-3.4	2.7		
-3.2	2.5		
-3.0	2.2		
-3.4		6.4	
-3.2		6.1	
-3.0		5.5	
-2.8		5.4	
-2.6		4.8	
-2.4		4.0	
-2.2		3.6	
-2.0		3.7	
-2.2		2.5	
-2.0		2.1	
-1.8			6.5
-1.6			6.3
-1.4			5.8
-1.2			5.4
-1.0			5.2
-1.2			4.2
-1.0			3.9
-1.2			3.9
-1.0			3.2
-0.8			3.0
-1.0			2.5
-0.5			
-0.2			
0.0			

Fig. 8.30

203270* 84E92860

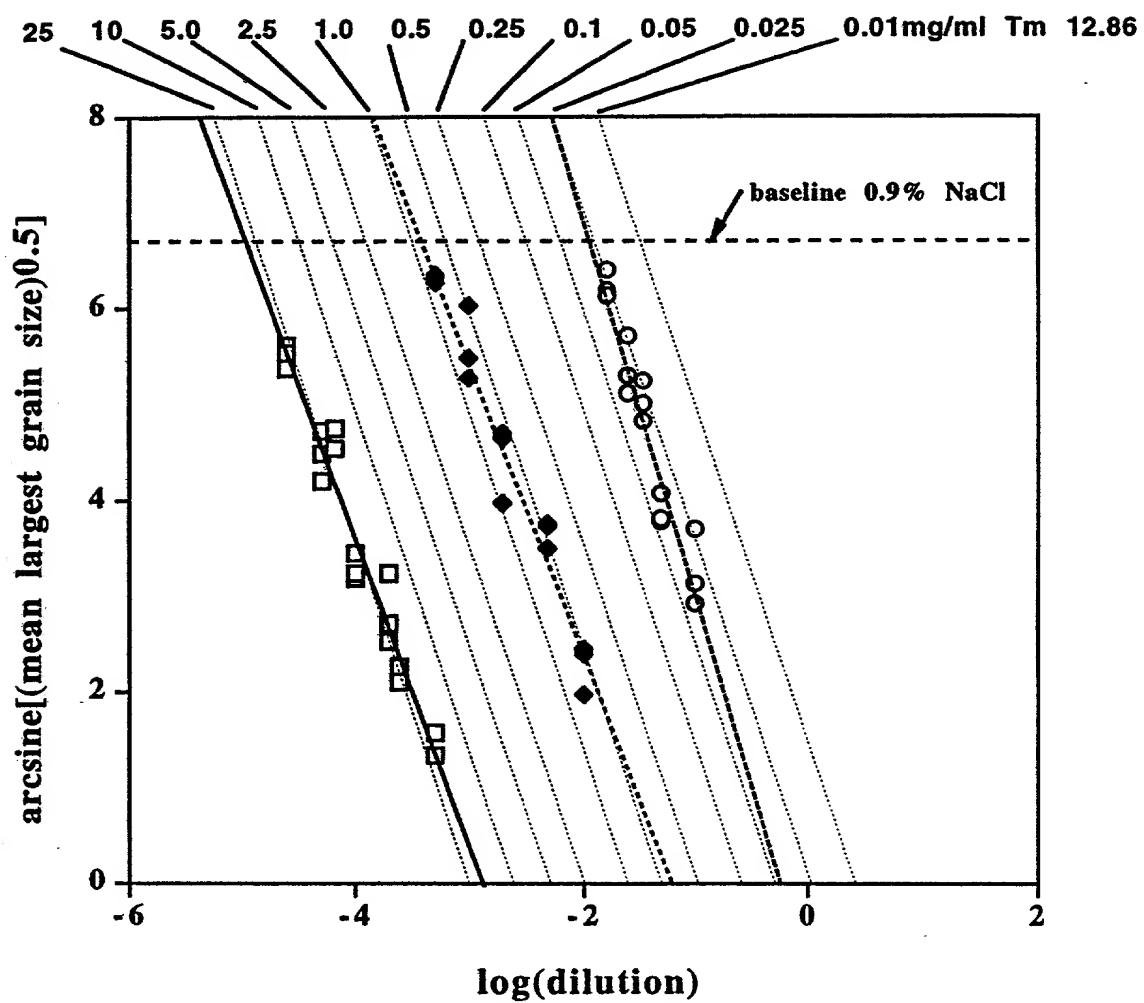


Fig. 8.31

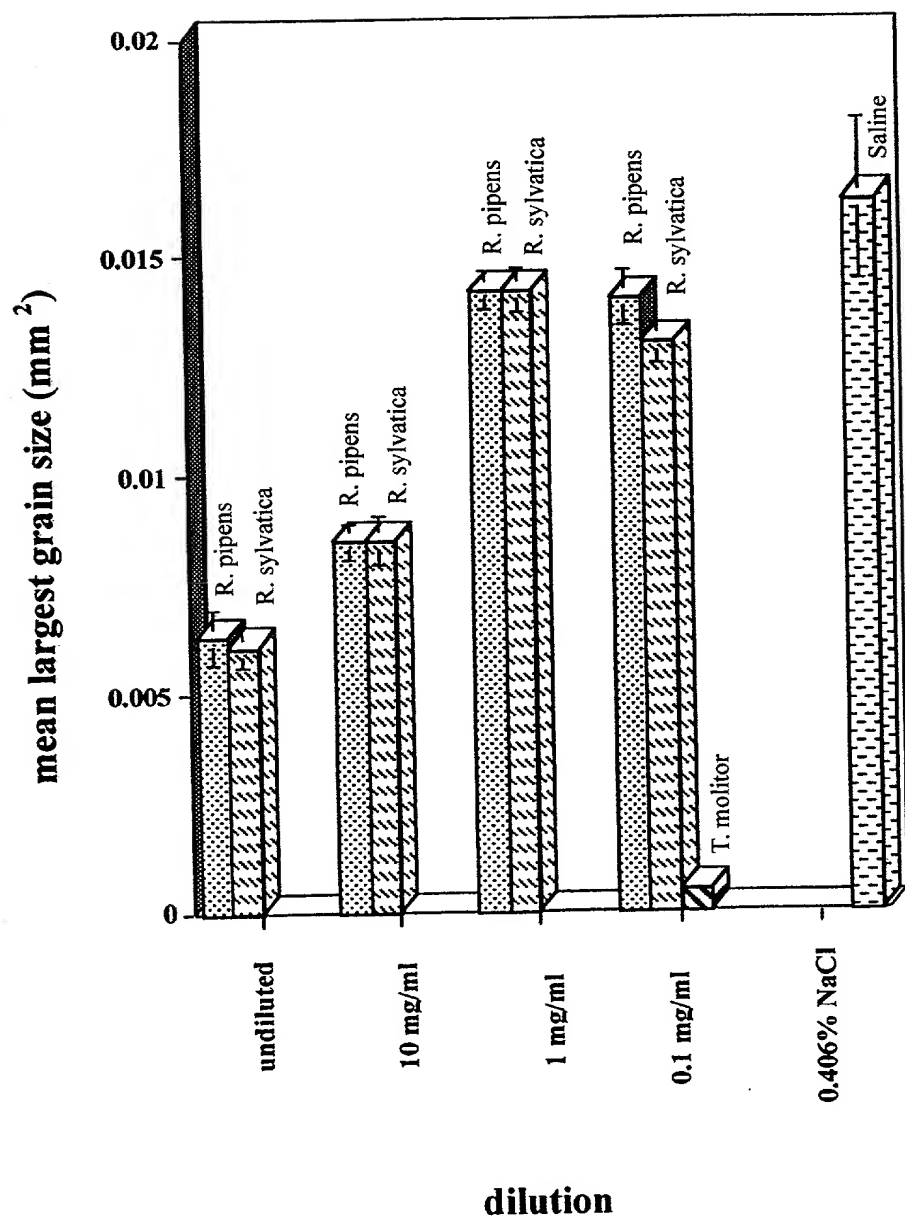


Fig. 8.32

202210-84E92850

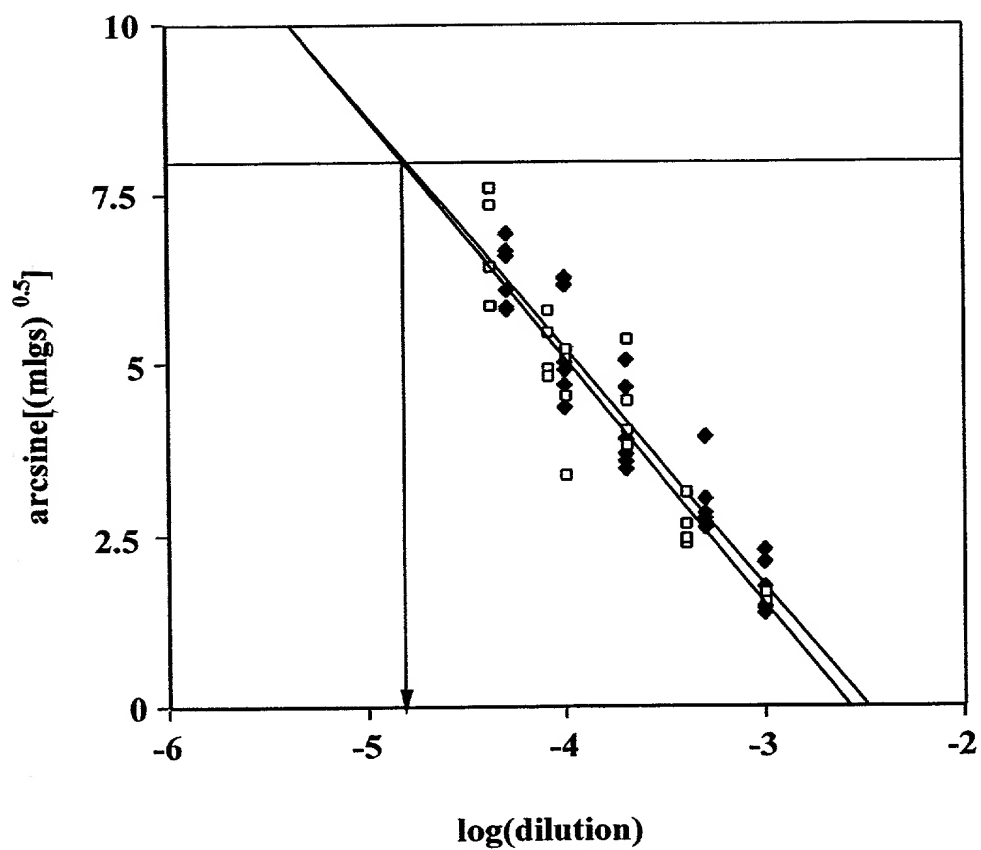


Fig. 8.33

203210* 64292860

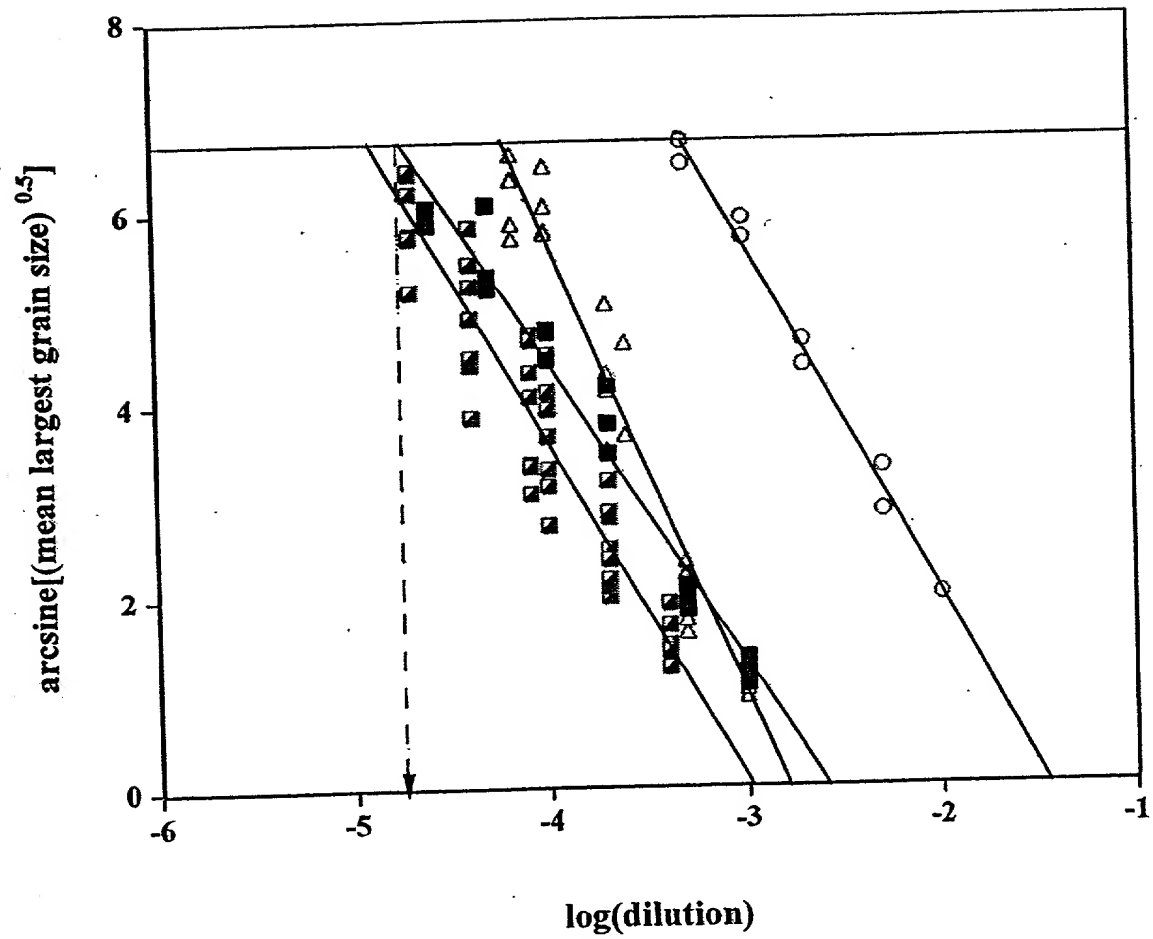


Fig. 8.34

208270-84892860

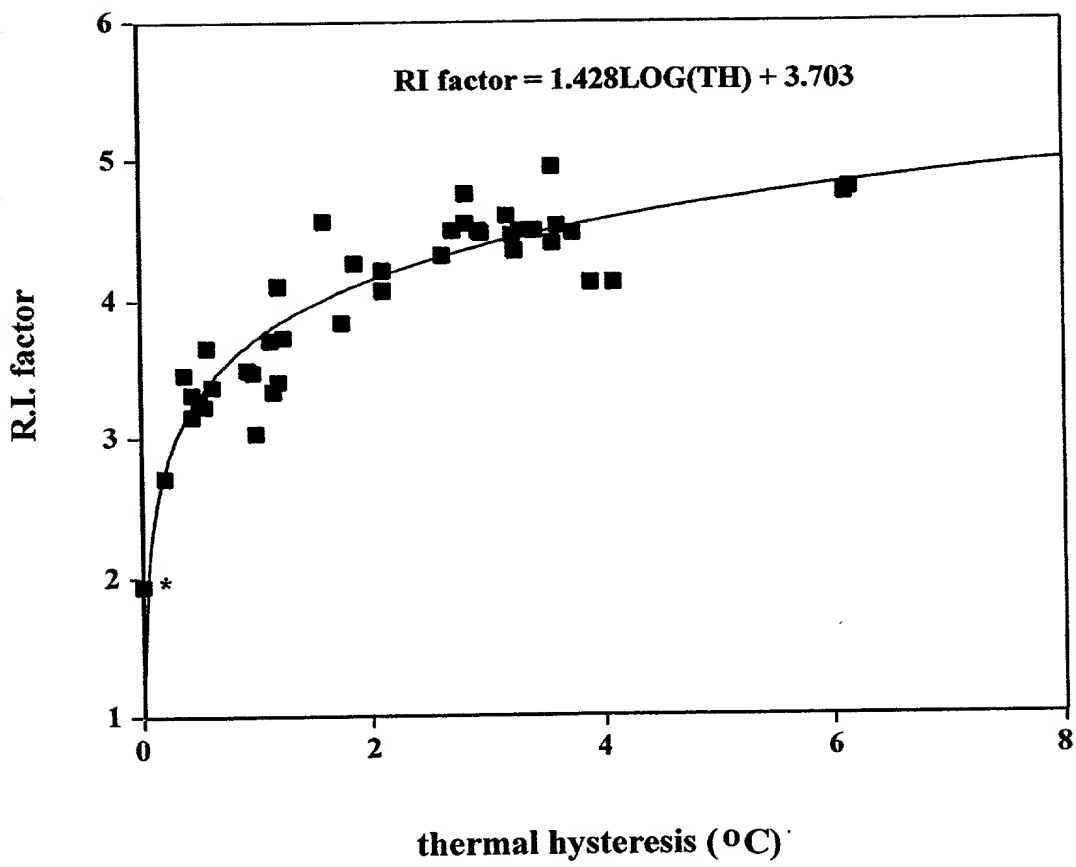


Fig. 8.35

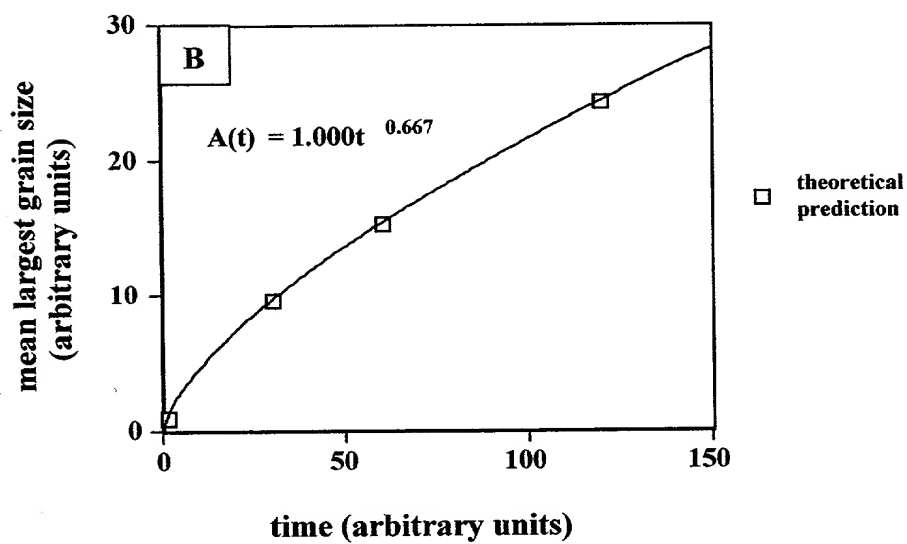
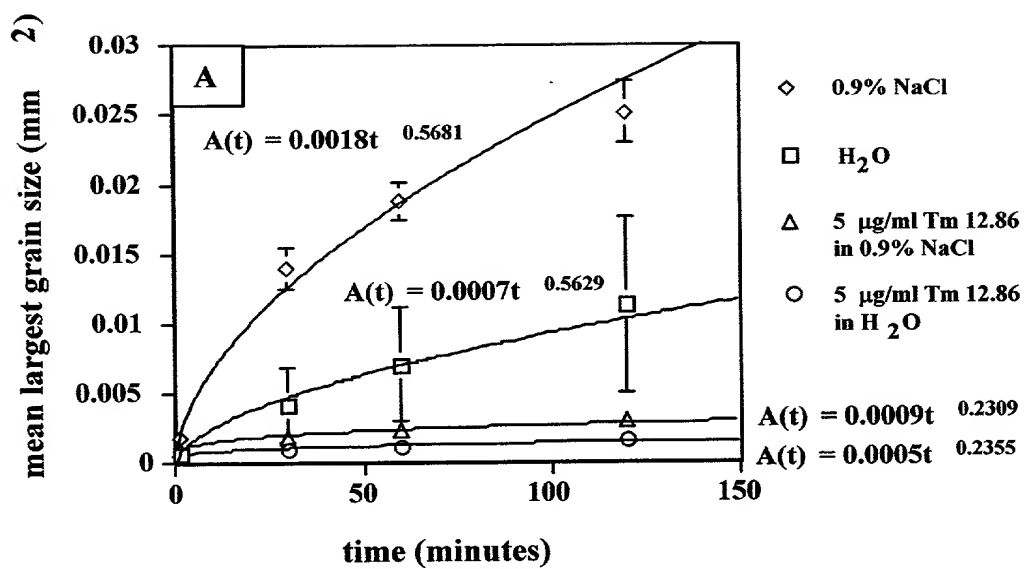


Fig. 8.36

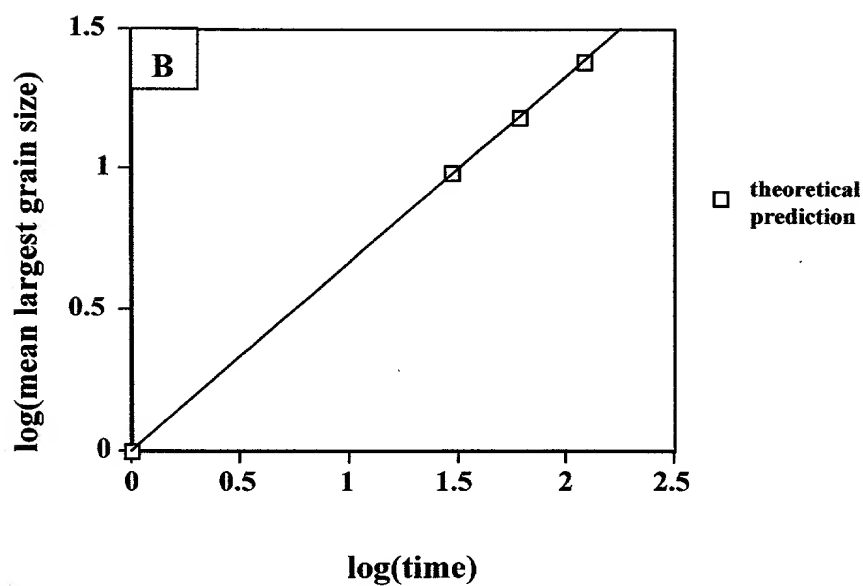
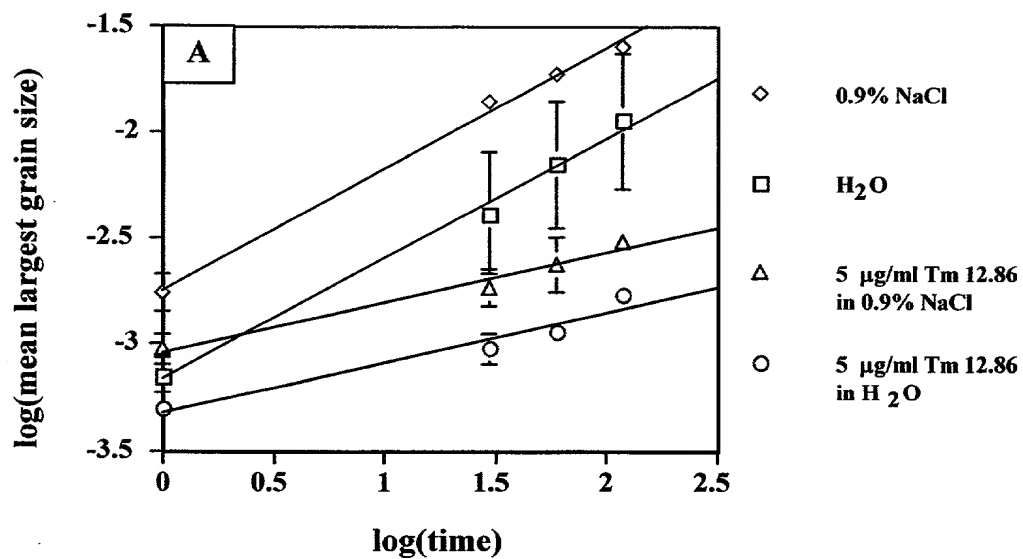
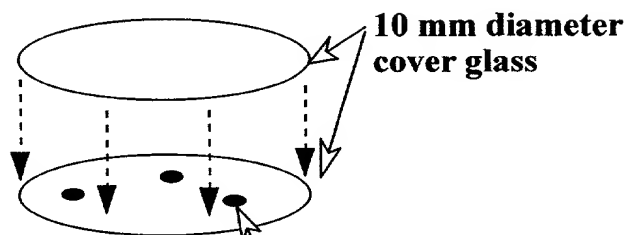


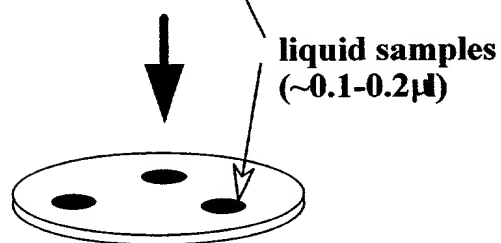
Fig. 8.37

"Sandwich" method of R.I. assessment

1.



2.



3. FREEZE ON ~ -80 C
ALUMINUM PLATE (~ 10 MIN.)



4. PLACE ON COLD STAGE,
ANNEAL AT -6 C UP TO
12+ HOURS

Fig. 8.38

00000 00000 00000

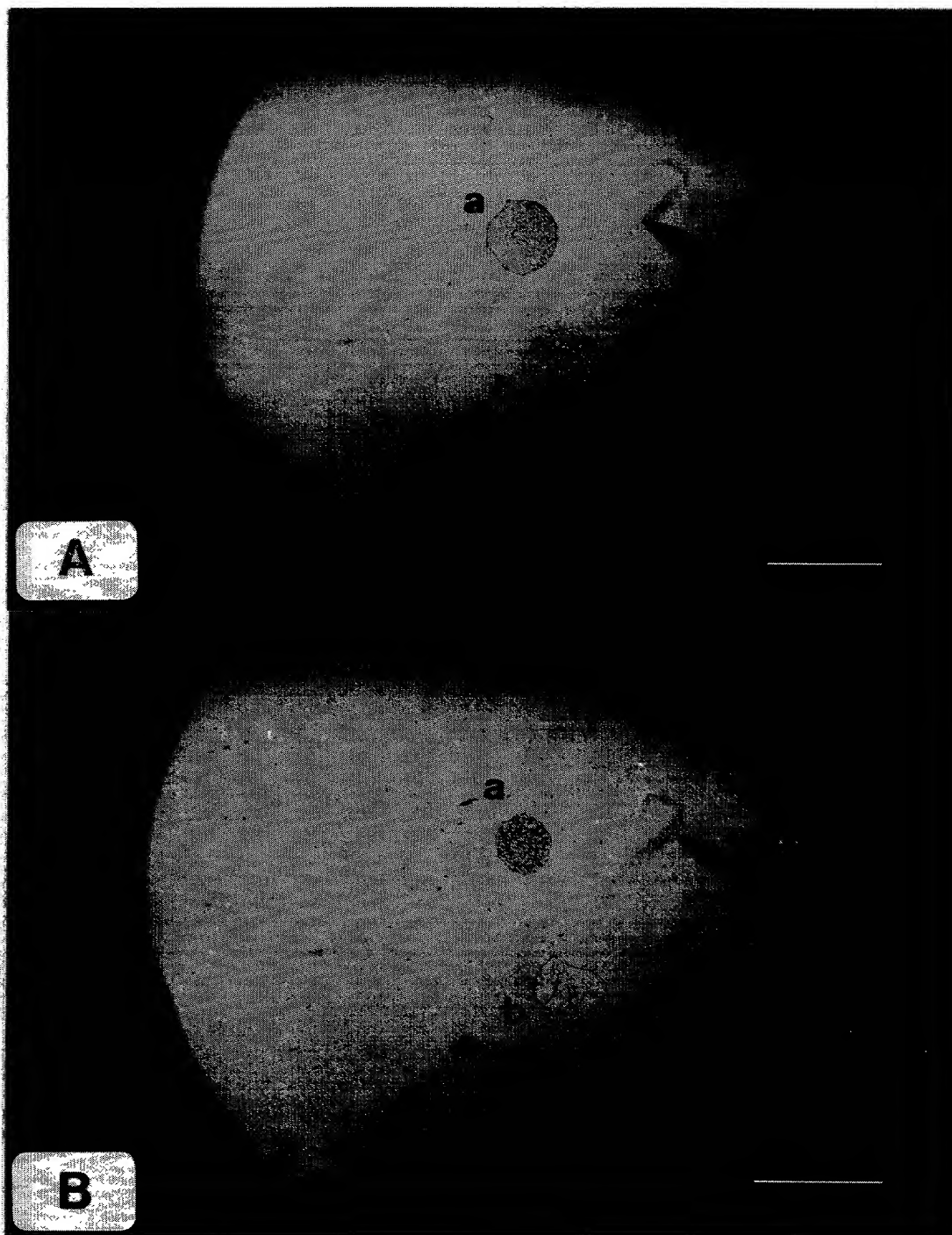


Fig. 8.39

203210 31.29.2860

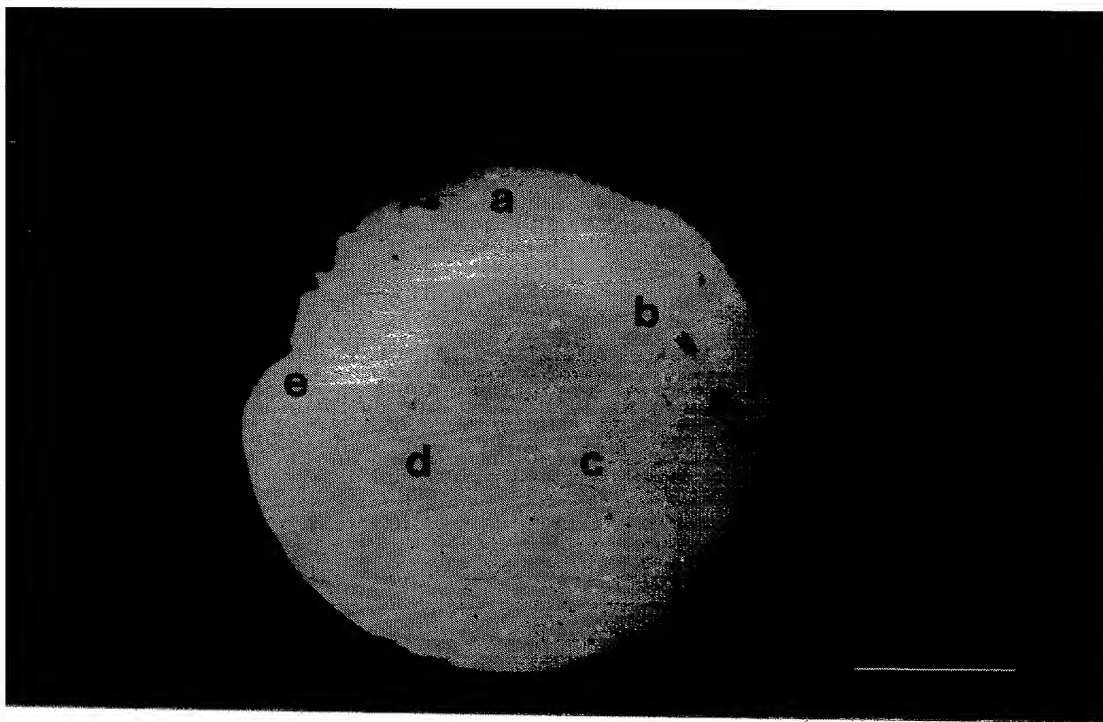


Fig. 8.40

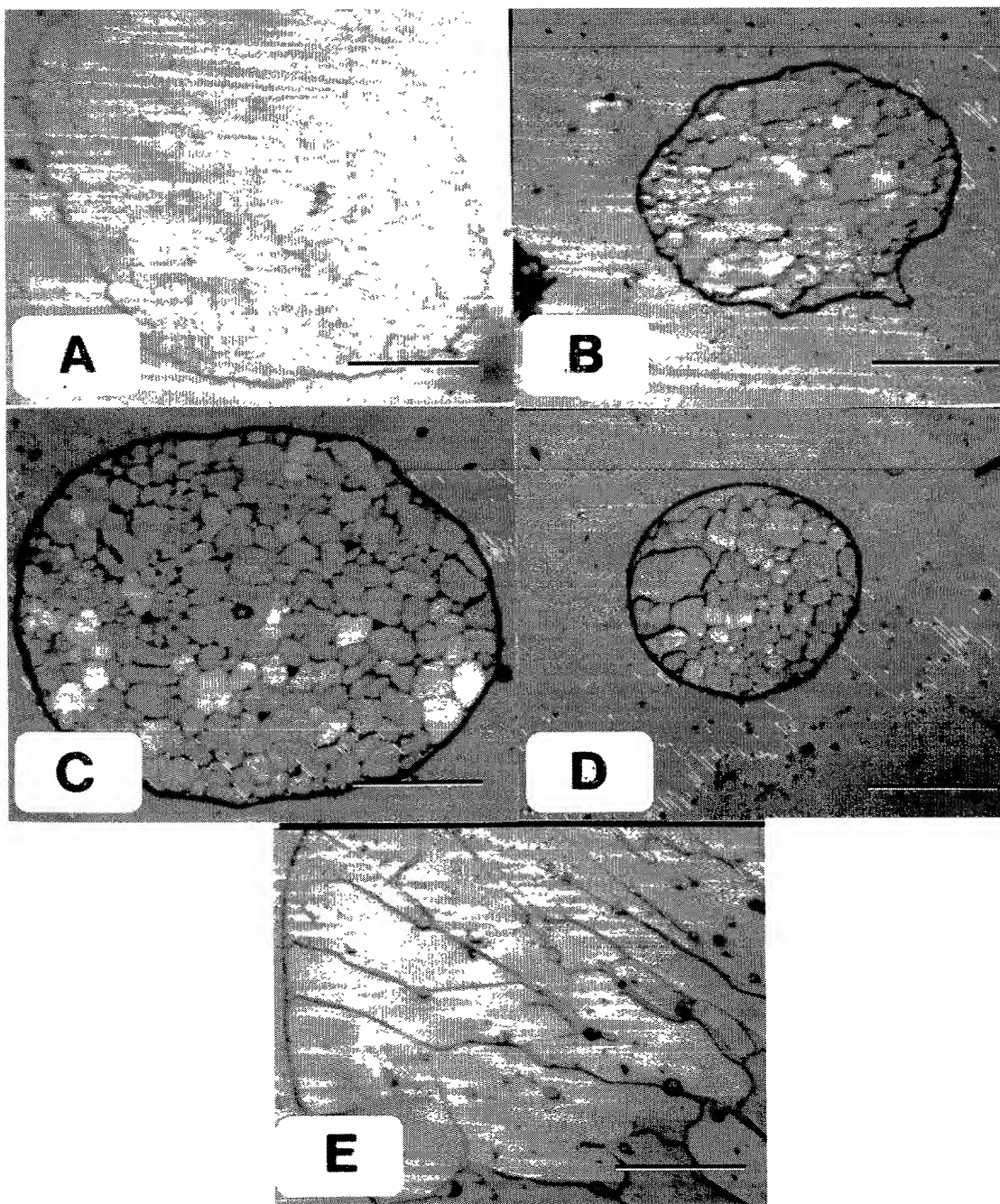


Fig. 8.41

A circular grid of 30 numbered squares, arranged in a 6x5 pattern. The squares are numbered 1 through 30, starting from the top left and moving right across each row. The grid is tilted slightly to the right. In the bottom left corner, there is a small square containing the letter 'A'.



Fig. 8.42

DNA sequence of Tm 13.17 cDNA clone

B	E
a	C
m	O
H	R
I	I

1 AGTGGATCCAAAGAATTCCGGCACGAGACTACTAAGATGAAGTTGCTCTGTTGTCTAATCT
M K L L C C L I S

61 CCCTCATTCTGTTGGTCCACAGTTCAGGCCCTGACCGAGGCACAAATTGAGAAACTGAACA
L I L L V T V Q A L T E A Q I E K L N K

121 AGATCAGCAAAAAATGTCAAAATGAAAGTGGAGTGTCTCGCAAGATGATCATAACCAAAGCTC
I S K K C Q N E S G V S Q E I I T K A R

181 GCAACGGTGAAGTGGGAGGACGATCCTAAACTGAAACGCCAAGTTTTTTGCGTGGCCAGGA
N G D W E D D P K L K R Q V F C V A R N

241 ACGCCGGTCTGGCCACGGAATCGGGAGAGGTGGTGGTTCGACGTGTTGAGGGAGAAGGTGA
A G L A T E S G E V V V D V L R E K V R

301 GGAAGGTCACTGACAACGACGAAGAAACTGAGAAAATCATCAATAAGTGGCCCGTCAAGA
K V T D N D E E T E K I I N K C A V K R

361 GAGATACTGTTGAAGAGACGGTGTTCATACTTTCAAATGTGTCATGAAAAACAAGCCAA
D T V E E T V F N T F K C V M K N K P K

421 AGTTCTCACCAGTTGATTGAACCAACCAGACTAGTAGATGGTTCAAATGGTGTGCTTTAC
F S P V D *

481 ATATAAAAAATAAAGTGTCTTCTGATGTAAAAAATAAAAAAAAAAAAAAAAAAACTCG
polyadenylation signal poly (A) tail (26)

537 AGAGTATTCTAGAGCGGCCGCGGGCCCATCGTTTCCACCC

Fig. 8.43

1 GGCACGAGCAAAAATGAAACTCCTCTTGTGCTTTGCGTTCGCCGCC
 M K L L L C F A F A A
 47 ATCGTCATCGGAGCTCAGGCTCTCACCGACGAACAGATACAGAAA
 P G
 I V I G A Q A L T D E Q I Q K
 92 AGGAACAAGATCAGCAAAGAATGCCAGCAGGTGTCCGGAGTGTCC
 Y
 G V S
 137 CAAGAAGACGATCGACAAAGTCCGCACAGGTGTCTTGGTCGATGAT
 Y
 Q E T I D K V R T G V L V D D
 182 CCCAAAATGAAGAAGCACGTCCTCTGCTTCTCGAAGAAAACCTGGA
 P K M K K H V L C F S K K T G
 226 GTGGCAACCGAAGCCGGAGACACCAATGTGGAGGTACTCAAAGCC
 V A T E A G D T N V E V L K A
 271 AAGCTGAAGCATGTGGCCAGCGACGAAGAGGTGGACAAGATCGTG
 K L K H V A S D E E V D K I V
 316 CAGAAGTGCGTGGTCAAGAAGGCCACACCAAGAGGAAACGGCTTAT
 P
 Q K C V V K K A T P E E T A Y
 361 GACACCTTCAAGTGTATTTACGACAGCAAACCTGATTTCTCTCCT
 P G
 D T F K C I Y D S K P D F S P
 406 ATTGATTAAATTGTTTTGTATTTGACTGAATTTTGACAATAAAGGT
 G
 I D
 451 ACTATCGTTATGTAAAAAAAAAAAAAAAAAAAAA
 polyadenylation signal

poly (A) tail

Fig. 8.44